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From: Seharaseyon, Jegatheesan
Sent: Monday, June 05, 2006 10:49 AM
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Subject: 10/063534

Please search SEQ ID NO: 30 in the pending and allowed databases.
Also please search with a word size of 6 amino acids.

Thanks

J. Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
Fax: (571)-273-0892

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search

NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: June 6, 2006, 21:26:54 ; Search time 16 Seconds
(without alignments)
52.766 Million cell updates/sec

Title: US-10-063-534-30

Perfect score: 73
Sequence: 1 MLLTLTLTLTLTKGSCLEW.....PAMTCQAQPRGEGKVDG 73

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 58871 seqs, 11565156 residues

Word size : 6

Total number of hits satisfying chosen parameters: 246

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- Published Applications_AA_New:*
- 1: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US09_NEW_PUB.pep:*
 - 2: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US06_NEW_PUB.pep:*
 - 3: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US07_NEW_PUB.pep:*
 - 4: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_NEW_PUB.pep:*
 - 5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
 - 6: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10_NEW_PUB.pep:*
 - 7: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_NEW_PUB.pep:*
 - 8: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	73	US-11-101-316-30	Sequence 30, Appl 1
2	9	12.3	294	US-10-953-349-25258	Sequence 25258, A
3	9	12.3	314	US-10-953-349-25257	Sequence 25257, A
4	9	12.3	515	US-10-953-349-21352	Sequence 21352, A
5	9	12.3	516	US-10-953-349-21351	Sequence 21351, A
6	9	12.3	521	US-10-953-349-21350	Sequence 21350, A
7	8	11.0	16	US-11-257-581-13	Sequence 13, Appl 1
8	8	11.0	173	US-11-293-697-3431	Sequence 3431, Ap
9	8	11.0	205	US-10-511-937-2938	Sequence 2938, Ap
10	8	11.0	208	US-10-953-349-15677	Sequence 15677, A
11	8	11.0	232	US-10-514-462-7	Sequence 7, Appl 1
12	8	11.0	234	US-10-196-749-482	Sequence 482, App
13	8	11.0	243	US-11-320-192-9	Sequence 9, Appl 1
14	8	11.0	243	US-11-320-192-12	Sequence 12, Appl 1
15	8	11.0	314	US-10-953-349-34590	Sequence 34590, A
16	8	11.0	338	US-11-140-450-95	Sequence 95, Appl 1
17	8	11.0	378	US-10-953-349-34588	Sequence 34588, A
18	8	11.0	397	US-11-244-452-7	Sequence 7, Appl 1
19	8	11.0	418	US-10-953-349-32813	Sequence 32813, A
20	8	11.0	467	US-10-196-749-16	Sequence 16, Appl 1
21	8	11.0	480	US-11-301-554-336	Sequence 336, App
22	8	11.0	487	US-10-196-749-230	Sequence 230, App
23	8	11.0	508	US-10-953-349-32268	Sequence 32268, A
24	8	11.0	521	US-10-953-349-32267	Sequence 32267, A
25	8	11.0	531	US-11-257-581-4	Sequence 4, Appl 1

26	8	11.0	531	US-11-257-581-5	Sequence 5, Appl 1
27	8	11.0	531	US-11-257-581-6	Sequence 6, Appl 1
28	8	11.0	538	US-11-140-450-37	Sequence 37, Appl 1
29	8	11.0	544	US-11-257-581-1	Sequence 1, Appl 1
30	8	11.0	544	US-11-257-581-2	Sequence 2, Appl 1
31	8	11.0	544	US-11-257-581-3	Sequence 3, Appl 1
32	8	11.0	721	US-11-293-697-3470	Sequence 3470, Ap
33	8	11.0	813	US-10-196-749-466	Sequence 466, App
34	8	11.0	837	US-10-196-749-454	Sequence 454, App
35	8	11.0	837	US-10-540-394-1	Sequence 1, Appl 1
36	8	11.0	837	US-10-540-394-4	Sequence 4, Appl 1
37	8	11.0	837	US-10-540-394-7	Sequence 7, Appl 1
38	8	11.0	837	US-10-540-394-10	Sequence 10, Appl 1
39	8	11.0	972	US-11-255-147-8	Sequence 8, Appl 1
40	8	11.0	1015	US-10-505-928-359	Sequence 359, App
41	8	11.0	4590	US-10-505-928-569	Sequence 569, App
42	7	9.6	69	US-10-953-349-36432	Sequence 36432, A
43	7	9.6	75	US-10-953-349-36431	Sequence 36431, A
44	7	9.6	82	US-10-953-349-28006	Sequence 28006, A
45	7	9.6	84	US-10-196-749-186	Sequence 186, App

ALIGNMENTS

RESULT 1
US-11-101-316-30
Sequence 30, Application US/11101316
Publication No. US20060099657A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIDOTES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
FILE REFERENCE: P323081C17C1
CURRENT APPLICATION NUMBER: US/11/101.316
PRIOR FILING DATE: 2005-04-06
PRIOR APPLICATION NUMBER: 10/063526
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 30
LENGTH: 73
TYPE: PRT
ORGANISM: Homo Sapien
US-11-101-316-30
Query Match 100.0%; Score 73; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 9.6e-62;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MLLTLTLTLTLTKGSCLEWGVAAQVSSATAPIRDMAFPPSPFICLPHPRAMTCQ 60
Db 1 MLLTLTLTLTLTKGSCLEWGVAAQVSSATAPIRDMAFPPSPFICLPHPRAMTCQ 60
Cy 61 AQRGEGEKVDG 73
Db 61 AQRGEGEKVDG 73
RESULT 2

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US-10-953-349-25258
; Sequence 25258, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25258
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (130)..(130)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (276)..(276)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: (278)..(278)
; LOCATION: (278)..(278)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-25258
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Query Match          12.3%; Score 9; DB 6; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 LLLTLLLL 10
         |||||
Db       11 LLLTLLLL 19
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RESULT 3
US-10-953-349-25257
; Sequence 25257, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25257
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (150)..(150)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1296)..(1296)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (298)..(298)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-25257
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Query Match          12.3%; Score 9; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 LLLTLLLL 10
         |||||
Db       31 LLLTLLLL 39
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RESULT 4
US-10-953-349-21352
; Sequence 21352, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21352
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21352
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Query Match          12.3%; Score 9; DB 6; Length 515;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      4 LTLTLLLL 12
         |||||
Db       17 LTLTLLLL 25
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RESULT 5
US-10-953-349-21351
; Sequence 21351, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21351
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-21351
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Query Match          12.3%; Score 9; DB 6; Length 516;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      4 LTLTLLLL 12
         |||||
Db       18 LTLTLLLL 26
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```
RESULT 6
US-10-953-349-21350
; Sequence 21350, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 21350
LENGTH: 521
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-21350

Query Match
Best Local Similarity 12.3%; Score 9; DB 6; Length 521;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LLLLLLLL 12
Db 23 LLLLLLLL 31

RESULT 7
US-11-257-581-13
Sequence 13, Application US/11257581
Publication No. US20060093614A1
GENERAL INFORMATION:
APPLICANT: Shaw, Gray D.
APPLICANT: Sako, Dianne S.
APPLICANT: Kumar, Ravindra
APPLICANT: Sullivan, Francis
APPLICANT: McDonagh, Tom
TITLE OF INVENTION: Platelet Glycoprotein IB Alpha Fusion Polypeptides and
TITLE OF INVENTION: Methods of Use Thereof
FILE REFERENCE: 22058-503
CURRENT APPLICATION NUMBER: US/11/257,581
PRIOR FILING DATE: 2005-10-24
PRIOR APPLICATION NUMBER: US/10/068,426
PRIOR FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/266,838
PRIOR FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (1)-(16)
OTHER INFORMATION: Signal Peptide
US-11-257-581-13

Query Match
Best Local Similarity 11.0%; Score 8; DB 7; Length 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LLLLLLLL 13
Db 3 LLLLLLLL 10

RESULT 8
US-11-293-697-3431
Sequence 3431, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
PRIOR FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3431
LENGTH: 173

TYPE: PRT
ORGANISM: Homo sapiens
US-11-293-697-3431

Query Match
Best Local Similarity 11.0%; Score 8; DB 7; Length 173;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LLLLLLLL 13
Db 13 LLLLLLLL 20

RESULT 9
US-10-511-937-2938
Sequence 2938, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
PRIOR FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2938
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2938

Query Match
Best Local Similarity 11.0%; Score 8; DB 6; Length 206;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LLLLLLLL 13
Db 38 LLLLLLLL 45

RESULT 10
US-10-953-349-15677
Sequence 15677, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1578PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
PRIOR FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 15677
LENGTH: 208
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-15677

Query Match 11.0%; Score 8; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLL 13
| | | | |
Db 84 LLLLLLLL 91

RESULT 11
US-10-514-462-7

; Sequence 7, Application US/10514462
; Publication No. US20060088909A1
; GENERAL INFORMATION:

; APPLICANT: Emory University
; TITLE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic
; FILE REFERENCE: 050508-2210
; CURRENT APPLICATION NUMBER: US/10/514,462
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: 60/381,557
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 232
; TYPE: PRT
; ORGANISM: extracellular coding domain of the FL gene
US-10-514-462-7

Query Match 11.0%; Score 8; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLL 13
| | | | |
Db 14 LLLLLLLL 21

RESULT 12
US-10-196-749-482

; Sequence 482, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P343081C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 482
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-482

Query Match 11.0%; Score 8; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLL 13
| | | | |
Db 19 LLLLLLLL 26

RESULT 13
US-11-320-192-9

; Sequence 9, Application US/11320192
; Publication No. US20060104973A1
; GENERAL INFORMATION:
; APPLICANT: He, Zhigang
; APPLICANT: Wang, Kevin C.
; APPLICANT: Kim, Jieun A.
; TITLE OF INVENTION: Reducing NGR-p75 Mediated Inhibition of Axon
; FILE REFERENCE: CMCC-1043
; CURRENT APPLICATION NUMBER: US/11/320,192
; CURRENT FILING DATE: 2005-12-27
; PRIOR APPLICATION NUMBER: US/10/211,157
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 243
; TYPE: PRT
; ORGANISM: mouse
US-11-320-192-9

Query Match 11.0%; Score 8; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLL 13
| | | | |
Db 6 LLLLLLLL 13

RESULT 14
US-11-320-192-12

; Sequence 12, Application US/11320192
; Publication No. US20060104973A1
; GENERAL INFORMATION:
; APPLICANT: He, Zhigang
; APPLICANT: Wang, Kevin C.
; APPLICANT: Kim, Jieun A.
; TITLE OF INVENTION: Reducing NGR-p75 Mediated Inhibition of Axon
; FILE REFERENCE: CMCC-1043
; CURRENT APPLICATION NUMBER: US/11/320,192
; CURRENT FILING DATE: 2005-12-27
; PRIOR APPLICATION NUMBER: US/10/211,157
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1

Fri Jun 9 11:07:57 2006

SEQ ID NO 12
LENGTH: 243
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-320-192-12

Query Match 11.0%; Score 8; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLL 13
|||
Db 6 LLLLLLL 13

RESULT 15
US-10-953-349-34590
Sequence 34590, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 34590
LENGTH: 314
TYPE: PRT
ORGANISM: Zea mays subsp. mays
US-10-953-349-34590

Query Match 11.0%; Score 8; DB 6; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLL 13
|||
Db 6 LLLLLLL 136

Search completed: June 6, 2006, 21:30:07
Job time : 16 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2006, 00:17:56 ; Search time 180 Seconds
(without alignments)
187.859 Million cell updates/sec

Perfect score: 73
Sequence: 1 MLLTLTLTLTLTKSCLEW.....PAMTCQAOPRGEKXVDG 73

Scoring table: OLIGO
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SUMMARIES

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17	73	100.0	73	3	US-10-015-519A-22
18	73	100.0	73	3	US-10-015-715A-22
19	73	100.0	73	3	US-10-007-236A-22
20	10	13.7	689	2	US-09-232-200-73
21	10	13.7	689	2	US-09-232-197-73
22	10	13.7	689	2	US-09-232-201-73
23	10	13.7	689	2	US-09-232-195-73
24	10	13.7	689	3	US-09-405-504A-73
25	9	12.3	21	1	US-07-715-397A-2
26	9	12.3	21	1	US-08-060-833-2

27	9	12.3	21	1	US-08-419-824-2	Sequence 2, Appl1
28	9	12.3	21	2	US-08-848-580-2	Sequence 2, Appl1
29	9	12.3	21	2	US-08-488-123-2	Sequence 2, Appl1
30	9	12.3	21	5	PCT-US92-04537-8	Sequence 8, Appl1
31	9	12.3	26	2	US-09-336-536-59	Sequence 59, Appl1
32	9	12.3	98	2	US-09-513-999C-4280	Sequence 4280, Ap
33	9	12.3	101	2	US-09-513-999C-4281	Sequence 4281, Ap
34	9	12.3	104	2	US-09-248-796A-27204	Sequence 27204, A
35	9	12.3	120	2	US-09-270-767-58991	Sequence 58991, A
36	9	12.3	131	2	US-08-938-548B-2	Sequence 2, Appl1
37	9	12.3	131	2	US-08-939-093A-2	Sequence 2, Appl1
38	9	12.3	131	2	US-09-211-823C-2	Sequence 2, Appl1
39	9	12.3	131	2	US-09-737-379A-2	Sequence 2, Appl1
40	9	12.3	213	2	US-09-336-536-58	Sequence 58, Appl1
41	9	12.3	229	2	US-09-270-767-43613	Sequence 43613, A
42	9	12.3	500	1	US-07-755-573C-8	Sequence 8, Appl1
43	9	12.3	500	2	US-09-519-878-2	Sequence 2, Appl1
44	9	12.3	520	2	US-09-949-016-10586	Sequence 10586, A
45	9	12.3	546	2	US-09-746-359A-37	Sequence 37, Appl1

ALIGNMENTS

RESULT 1
US-10-012-231A-22
Sequence 22, Application US/10012231A
Patent No. 6924355
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P28301C23
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: sig.peptide
FEATURE:
LOCATION: 1-15
NAME/KEY: misc.feature
LOCATION: 3-18
OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-231A-22
Query Match 100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MLLTLTLTLTLKSGCLEWGVGAQVSSATDAPTRDAFPSPFCLTPHPAMTCGQ 60
1 MLLTLTLTLTLKSGCLEWGVGAQVSSATDAPTRDAFPSPFCLTPHPAMTCGQ 60
61 AOPRGEKVGKVG 73

Db 61 AOPRGECEKVG DG 73

RESULT 2

US-10-015-389A-22
Sequence 22, Application US/10015389A
Patent No. 6936436
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830P1C48
CURRENT APPLICATION NUMBER: US/10/015,389A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3-18
OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-389A-22

Query Match 100.0%; Score 73; DB 2; Length 73;

Best Local Similarity 100.0%; Pred. No. 2,7e-65; Mismatches 0; Indels 0; Gaps 0;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLTLLTLLLLKSGCLEWGLVGAQKVSATDAPRIDMAFPSPFLCLPHRPAMTCSQ 60
Db 1 MLLTLLTLLLLKSGCLEWGLVGAQKVSATDAPRIDMAFPSPFLCLPHRPAMTCSQ 60

QY 61 AOPRGECEKVG DG 73
Db 61 AOPRGECEKVG DG 73

RESULT 3

US-10-006-768A-22
Sequence 22, Application US/10006768A
Patent No. 6936697
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2830P1C10

CURRENT APPLICATION NUMBER: US/10/006,768A

CURRENT FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 477

Prior Application removed - See File Wrapper or Palm

SEQ ID NO 22

LENGTH: 73

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: sig_peptide

LOCATION: 1-15

OTHER INFORMATION: Signal peptide.

FEATURE:

NAME/KEY: misc_feature

LOCATION: 3-18

OTHER INFORMATION: Growth factor and cytokines receptors family.

US-10-006-768A-22

Query Match 100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2,7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLTLLTLLLLKSGCLEWGLVGAQKVSATDAPRIDMAFPSPFLCLPHRPAMTCSQ 60
Db 1 MLLTLLTLLLLKSGCLEWGLVGAQKVSATDAPRIDMAFPSPFLCLPHRPAMTCSQ 60

QY 61 AOPRGECEKVG DG 73
Db 61 AOPRGECEKVG DG 73

RESULT 4

US-10-015-671A-22
Sequence 22, Application US/10015671A
Patent No. 6946263
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830P1C47
CURRENT APPLICATION NUMBER: US/10/015,671A
CURRENT FILING DATE: 2001-12-11
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
FEATURE:
NAME/KEY: misc_feature

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; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-671A-22

Query Match      100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLTTLTLLLLKSGCLEWGLVGAQKVSSATDAPIRDMAFPPSPFLCLLPHRPMATCSQ 60
Db 1 MLLTTLTLLLLKSGCLEWGLVGAQKVSSATDAPIRDMAFPPSPFLCLLPHRPMATCSQ 60

Qy 61 AOPRGEGEKVGDG 73
Db 61 AOPRGEGEKVGDG 73

RESULT 5
US-10-015-393A-22
; Sequence 22, Application US/10015393A
; Patent No. 6951737
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; PRIOR FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-393A-22

Query Match      100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLTTLTLLLLKSGCLEWGLVGAQKVSSATDAPIRDMAFPPSPFLCLLPHRPMATCSQ 60
Db 1 MLLTTLTLLLLKSGCLEWGLVGAQKVSSATDAPIRDMAFPPSPFLCLLPHRPMATCSQ 60

Qy 61 AOPRGEGEKVGDG 73
Db 61 AOPRGEGEKVGDG 73

RESULT 6
US-10-011-833A-22
; Sequence 22, Application US/10011833A
```

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; Patent No. 6951920
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C22
; CURRENT APPLICATION NUMBER: US/10/011,833A
; PRIOR FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-011-833A-22

Query Match      100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLTTLTLLLLKSGCLEWGLVGAQKVSSATDAPIRDMAFPPSPFLCLLPHRPMATCSQ 60
Db 1 MLLTTLTLLLLKSGCLEWGLVGAQKVSSATDAPIRDMAFPPSPFLCLLPHRPMATCSQ 60

Qy 61 AOPRGEGEKVGDG 73
Db 61 AOPRGEGEKVGDG 73

RESULT 7
US-10-006-041A-22
; Sequence 22, Application US/10006041A
; Patent No. 6951921
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A
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;; CURRENT FILING DATE: 2001-12-06
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 22
;; LENGTH: 73
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 1-15
;; OTHER INFORMATION: Signal peptide.
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 3-18
;; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-006-041A-22

Query Match 100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2,7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTTLLTLLLLKSGCLEWGLVGAOKVSSATDAPIRDMAFPPSPFLCLLPHRPMTCGQ 60
DB 1 MLTTLLTLLLLKSGCLEWGLVGAOKVSSATDAPIRDMAFPPSPFLCLLPHRPMTCGQ 60

QY 61 AOPRGEGERKVGDG 73
DB 61 AOPRGEGERKVGDG 73

RESULT 8
US-10-012-064A-22
; Sequence 22, Application US/10012064A
; Patent No. 6953841
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC19
; CURRENT APPLICATION NUMBER: US/10/012,064A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598

;; PRIOR FILING DATE: 1998-09-09
;; Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 22
;; LENGTH: 73
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 1-15
;; OTHER INFORMATION: Signal peptide.
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 3-18
;; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-064A-22

Query Match 100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2,7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTTLLTLLLLKSGCLEWGLVGAOKVSSATDAPIRDMAFPPSPFLCLLPHRPMTCGQ 60
DB 1 MLTTLLTLLLLKSGCLEWGLVGAOKVSSATDAPIRDMAFPPSPFLCLLPHRPMTCGQ 60

QY 61 AOPRGEGERKVGDG 73
DB 61 AOPRGEGERKVGDG 73

RESULT 9
US-10-015-392A-22
; Sequence 22, Application US/10015392A
; Patent No. 6972186
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598

;; PRIOR FILING DATE: 1998-09-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 22
;; LENGTH: 73
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig peptide
;; LOCATION: 1-15
;; OTHER INFORMATION: Signal peptide.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 3-18
;; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-392A-22

Query Match 100.0%; Score 73; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 2,7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLTLTLLLLLLKSGCLEMGLVGAQKVSSATDAPIRDMAFPPSPFLCLPHRPAMTCQ 60
Db 1 MLTLTLLLLLLKSGCLEMGLVGAQKVSSATDAPIRDMAFPPSPFLCLPHRPAMTCQ 60

Qy 61 AOPRGEKGVGDG 73
Db 61 AOPRGEKGVGDG 73

RESULT 10
US-10-011-795B-22
;; Sequence 22, Application US/10011795B
;; Patent No. 7012131

;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eaton, Dan I.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Guiney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2830P1C25
;; CURRENT APPLICATION NUMBER: US/10/011,795B
;; PRIOR FILING DATE: 2001-12-07
;; PRIOR APPLICATION NUMBER: 60/098716
;; PRIOR FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: 60/098723
;; PRIOR FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: 60/098749
;; PRIOR FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: 60/098750
;; PRIOR FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: 60/098803
;; PRIOR FILING DATE: 1998-09-02
;; PRIOR APPLICATION NUMBER: 60/098821
;; PRIOR FILING DATE: 1998-09-02
;; PRIOR APPLICATION NUMBER: 60/098843
;; PRIOR FILING DATE: 1998-09-02
;; PRIOR APPLICATION NUMBER: 60/099536
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099596
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099598

;; PRIOR FILING DATE: 1998-09-09
;; Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 22
;; LENGTH: 73
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig peptide
;; LOCATION: 1-15
;; OTHER INFORMATION: Signal peptide.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 3-18
;; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-011-795B-22

Query Match 100.0%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 2,7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLTLTLLLLLLKSGCLEMGLVGAQKVSSATDAPIRDMAFPPSPFLCLPHRPAMTCQ 60
Db 1 MLTLTLLLLLLKSGCLEMGLVGAQKVSSATDAPIRDMAFPPSPFLCLPHRPAMTCQ 60

Qy 61 AOPRGEKGVGDG 73
Db 61 AOPRGEKGVGDG 73

RESULT 11
US-10-015-386A-22
;; Sequence 22, Application US/10015386A
;; Patent No. 7022498

;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eaton, Dan I.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Guiney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2830P1C25
;; CURRENT APPLICATION NUMBER: US/10/015,386A
;; PRIOR FILING DATE: 2001-12-12
;; Prior Application removed - See File Wrapper or Palm
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 22
;; LENGTH: 73
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig peptide
;; LOCATION: 1-15
;; OTHER INFORMATION: Signal peptide.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 3-18
;; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-386A-22

Query Match 100.0%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 2,7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      1 MLTLTLLLTLLKSGSCLEWGLVGAQKVSSATDADIRDAFPFPPSFLCLPHRPAMTCGQ 60
        |||
DB      1 MLLTLLTLLLTLLKSKSCLEWGLVGAKVSSATDADIRDAFPFPPSFLCLPHRPAMTCGQ 60
        |||

OY      61 AOPRGEGERKVDG 73
        |||
DB      61 AOPRGEGERKVDG 73
        |||

RESULT 12
US-10-012-121A-22
; Sequence 22, Application US/10012121A
Patent No. 7022817
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC20
CURRENT FILING DATE: 2001-12-07
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3-18
OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-121A-22

Query Match          100.0%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY      1 MLLTLLTLLLTLLKSGSCLEWGLVGAQKVSSATDADIRDAFPFPPSFLCLPHRPAMTCGQ 60
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DB      1 MLLTLLTLLLTLLKSKSCLEWGLVGAKVSSATDADIRDAFPFPPSFLCLPHRPAMTCGQ 60
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OY      61 AOPRGEGERKVDG 73
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DB      61 AOPRGEGERKVDG 73
        |||

RESULT 13
US-10-006-485A-22
; Sequence 22, Application US/10006485A
Patent No. 7026448
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrara, Napoleone

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Fri Jun 9 11:07:57 2006

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 PRIOR APPLICATION NUMBER: 60/106023
 PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 73; DB 3; Length 73;
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 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MLTLTLLLLLLKSGCLWGLVGAQKVSATDAPRIDMAFFPPSPCLLPHRAMTCSQ 60
 Oy 61 AOPRGEKVG DG 73
 Db 61 AOPRGEKVG DG 73

RESULT 14
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 Sequence 22, Application US/10006746A
 Patent No. 7026449
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C5
CURRENT APPLICATION NUMBER: US/10/006,746A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/098716
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; PRIOR FILING DATE: 1998-10-28

Query Match      100.0%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MLTTLTLLTLLKSGCLEWGLVGAQKVSSATDAPIRDMAFFPPSFLCLLPHRPAMTCSQ 60

OY      61 AQRGEGEKVGDG 73
Db      61 AQRGEGEKVGDG 73

RESULT 15
US-10-012-752A-22
; Sequence 22, Application US/10012752A
; Patent No. 7026455
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
```

```
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C24
; CURRENT APPLICATION NUMBER: US/10/012,752A
; CURRENT FILING DATE: 2002-06-25
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 22
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
; US-10-012-752A-22
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Query Match      100.0%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 MLTTLTLLTLLKSGCLEWGLVGAQKVSSATDAPIRDMAFFPPSFLCLLPHRPAMTCSQ 60
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OY      61 AQRGEGEKVGDG 73
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Job time : 51 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 21:06:23 ; Search time 293 Seconds
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230.465 Million cell updates/sec

Title: US-10-063-534-30

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Searched: 2849598 seqs, 925015592 residues

Word size : 6

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1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	10	13.7	338	2	O3YP28 UTA STANBNU
4	10	13.7	341	2	O3YP32 UTA STANBNU
5	10	13.7	343	2	O3YP31 UTA STANBNU
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7	10	13.7	379	1	CYB BRAID
8	10	13.7	418	2	O3UNCG MOUSE
9	10	13.7	689	1	SZ7A5 MOUSE
10	9	12.3	39	2	O5R588 PONY
11	9	12.3	52	2	O4X6W7 PLACH
12	9	12.3	61	2	O3R079 XYLAFA
13	9	12.3	75	2	O8K4W3 MOUSE
14	9	12.3	96	2	O7NE75 GLOVI
15	9	12.3	99	2	O6MK16 BOVIN
16	9	12.3	116	2	O9EMPI ANEPV
17	9	12.3	125	2	O6IKC7 DROME
18	9	12.3	131	1	O6IKC7 DROME
19	9	12.3	131	1	O6IKC7 DROME
20	9	12.3	133	2	O5UG15 HUMAN
21	9	12.3	146	2	O2KSP5 ADE04
22	9	12.3	152	2	O7R117 GTRALA
23	9	12.3	159	2	O5S9C1 CANAL
24	9	12.3	161	2	O4ALY9 9CHLB
25	9	12.3	182	2	O3GK41 CHLVI
26	9	12.3	184	2	O5S9F3 CANAL
27	9	12.3	189	2	O8BLE9 MOUSE
28	9	12.3	199	2	O8IWT1 HUMAN
29	9	12.3	200	2	O496B3 HUMAN
30	9	12.3	208	1	YHNN_ECOS7
31	9	12.3	208	1	YHNN_ECOS6

32	9	12.3	208	1	YHNN_ECOS1	Poadj2 escherichia
33	9	12.3	208	1	YHNN_SHIFL	Poadj2 shigella fl
34	9	12.3	208	2	O3IVF8 SHIBS	O3IVF8 shigella bo
35	9	12.3	208	2	O3YMG0 SHISS	O3YMG0 shigella so
36	9	12.3	208	2	O2MTD1 ECOLI	O2MTD1 escherichia
37	9	12.3	230	2	O54UQ3 DICDI	O54UQ3 dictyostel
38	9	12.3	235	2	O8BJ86 MOUSE	O8BJ86 mus musculu
39	9	12.3	235	2	O8D710 MOUSE	O8D710 m adult mal
40	9	12.3	236	2	O91Z37 MOUSE	O91Z37 mus musculu
41	9	12.3	261	2	O4TEX9 TETNG	O4TEX9 tetradon n
42	9	12.3	311	2	O8IWT2 HUMAN	O8IWT2 homo sapien
43	9	12.3	313	2	O86YW5 HUMAN	O86YW5 homo sapien
44	9	12.3	381	2	O3O428 CANFA	O3O428 canis faml1
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ALIGNMENTS

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DT	05-JUL-2004, integrated into UniprotKB/TREMBL.					
DT	05-JUL-2004, sequence version 1.					
DT	07-FEB-2006, entry version 7.					
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GN	ORFNames=UNQ471;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;					
OC	Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;					
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RA	Chen Y., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,					
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RA	Vandena R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,					
RA	Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,					
RA	Wood W.I., Godowski P.J., Gray A.M.;					
RT	"The secreted protein discovery initiative (SPDI), a large-scale					
RT	effort to identify novel human secreted and transmembrane proteins: a					
RT	bioinformatics assessment."					
RL	Genome Res. 13:2265-2270(2003).					
CC	-----					
CC	Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms					
CC	Distributed under the Creative Commons Attribution-NonDerivs license					
CC	-----					
DR	EMBL; AY358657; AA089020.1; -; mRNA.					
DR	SEQUENCE 73 AA; 7879 MW; A99C96797BC4D91 CRC64;					
Query Match						
Best local Similarity		100.0%;	Score 73;	DB 2;	Length 73;	
Matches		73;	Conservative	0;	Mismatches	0;
					Indels	0;
					Gaps	0;
OY	1	MLLTLLTLLLLKSGSCLEWLVGAQKVSATDAPIRDMAFPPSPFLCLPFRPAMTCSQ	60			
DB	1	MLLTLLTLLLLKSGSCLEWLVGAQKVSATDAPIRDMAFPPSPFLCLPFRPAMTCSQ	60			
OY	61	AQPRGEGKVDG 73				
DB	61	AQPRGEGKVDG 73				
RESULT 2						
ID	O3YP30_UTAST	PRELIMINARY;	PRT;	337 AA.		
AC	O3YP30:					

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DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Cytochrome b (Fragment).
GN Name=cytb;
OS Uta stansburiana (Side-blotched lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX NCBI_TaxID=43653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ROM 37152;
RA Lindell J., Murphy R.W.;
RT "Simple identification of divergent mtDNA haplotypes with MAMA.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -1- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome b family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; DQ001863; AA220708.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR005798; Cytb_b6_N.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00033; Cytochrom_B_C; 1.
DR Pfam; PF00033; Cytochrom_B_N; 1.
DR PROSITE; PS51003; CYTB_CTER; 1.
DR PROSITE; PS51002; CYTB_NTER; 1.
DR Electron transport; Heme; Iron; Membrane; Metal-binding;
KW Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT NON TER
SQ SEQUENCE 337 AA; 38057 MW; 63C33F43B2B5B35 CRC64;

Query Match 13.7%; Score 10; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLLTLLLLL 11
Db 191 LLLTLLLLL 200

RESULT 3
Q3YP29_UTAST PRELIMINARY; PRT; 338 AA.
AC Q3YP29;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Cytochrome b (Fragment).
GN Name=cytb;
OS Uta stansburiana (Side-blotched lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX NCBI_TaxID=43653;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=ROM 37123;
RA Lindell J., Murphy R.W.;
RT "Simple identification of divergent mtDNA haplotypes with MAMA.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -1- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome b family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; DQ001864; AA220709.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005746; C:mitochondrial electron transport chain; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR005798; Cytb_b6_N.
DR InterPro; IPR005797; Cytb_b6_N.
DR Pfam; PF00033; Cytochrom_B_C; 1.
DR Pfam; PF00033; Cytochrom_B_N; 1.
DR PROSITE; PS51003; CYTB_CTER; 1.
DR PROSITE; PS51002; CYTB_NTER; 1.
DR Electron transport; Heme; Iron; Membrane; Metal-binding;
KW Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT NON TER
SQ SEQUENCE 338 AA; 37974 MW; 4B90C68A5DB2AD CRC64;

Query Match 13.7%; Score 10; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLLTLLLLL 11
Db 192 LLLTLLLLL 201

RESULT 4
Q3YP32_UTAST PRELIMINARY; PRT; 341 AA.
AC Q3YP32;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Cytochrome b (Fragment).
GN Name=cytb;
OS Uta stansburiana (Side-blotched lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.
OX NCBI_TaxID=43653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ROM 37151;
RA Lindell J., Murphy R.W.;
RT "Simple identification of divergent mtDNA haplotypes with MAMA.";
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis (By similarity).
CC -1- COFACTOR: Binds 2 heme groups noncovalently (By similarity).
CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome b family.
CC -----

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DR	GO; GO:0006118; P:electron transport; IEA.
DR	InterPro; IPR005798; Cytb_b6_C.
DR	InterPro; IPR005797; Cytb_b6_N.
DR	Pfam; PF00032; Cytochrom_B_C; 1.
DR	Pfam; PF00033; Cytochrom_B_N; 1.
DR	PROSITE; PSS1003; CYTB_CTER; 1.
DR	PROSITE; PSS1002; CYTB_NTER; 1.
KW	Electron transport; Heme; Iron; Membrane; Metal-binding;
KW	Mitochondrion; Respiratory chain; Transmembrane; Transport.
FT	NON_TER 1
SO	SEQUENCE 343 AA; 3875 MW; 9045C18C0B1EC27 CRC64;
Query Match	13.7%; Score 10; DB 2; Length 343;
Best Local Similarity	100.0%; Pred. No. 0.95;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
DY	2 LLLTLLLLL 11
Db	197 LLTLTLLL 206
RESULT 6	
O3YP37_UTAST	
ID O3YP37_UTAST PRELIMINARY; PRM; 347 AA.	
AC Q3YP37;	
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.	
DT 27-SEP-2005, sequence version 1.	
DT 07-FEB-2006, entry version 6.	
DE Cytochrome b (Fragment).	
CN Name=cytb;	
OS Uta stansburiana (Side-blotched lizard).	

Query Match 13.7%; Score 10; DB 2; Length 347;
 Best Local Similarity 100.0%; Pred. No. 0.95;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LLLTLLLLL 11
 DB 201 LLLTLLLLL 210

RESULT 7

CYB_BRAID STANDARD; PRT; 379 AA.
 ID CYB_BRAID
 AC O6ELM3;
 DT 15-MAR-2005, integrated into UniProtKB/Swiss-Prot.
 DT 16-AUG-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Cytochrome b.
 GN Name=MT-CYB; Synonyms=COB, CYTB, MTCYB;
 OS Brachylagus idahoensis (Pygmy rabbit).
 OG Mitochondrion.
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Brachylagus.
 OX NCBI_TaxID=48083;
 RN [1]

NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RP PubMed=15503672; DOI=10.1080/10635150490445715;

RA Matche C.A., van Vuuren B.J., Bell D., Robinson T.J.;

RT "A molecular supermatrix of the rabbits and hares (Leporidae) allows for the identification of five intercontinental exchanges during the

RT Miocene."

RL Syst. Biol. 53:433-447(2004).

CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase complex (complex III or cytochrome b-c1 complex), which is a respiratory chain that generates an electrochemical potential

CC coupled to ATP synthesis (By similarity).

CC -1- COFACTOR: Binds 2 heme groups noncovalently (By similarity).

CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,

CC cytochrome c1 and the Rieske protein (By similarity).

CC -1- MISCELLANEOUS: Heme 1 (or BL or b562) is low-potential and absorbs at about 562 nm, and heme 2 (or BH or b566) is high-potential and

CC absorbs at about 566 nm (By similarity).

CC -1- SIMILARITY: Belongs to the cytochrome b family.

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CC -----

CC EMBL: AY292721; AAS54917.1; -; Genomic_DNA.

DR SMR; Q6ELM3; 2-379.

DR InterPro; IPR005798; Cytb_b6_C.

DR InterPro; IPR005797; Cytb_b6_N.

DR Pfam; PF00033; Cytochrom_B_C1.

DR Pfam; PF00033; Cytochrom_B_N; 1.

DR PROSITE; PS51003; CYTB_CTER; 1.

DR PROSITE; PS51002; CYTB_NTER; 1.

KW Electron transport; Heme; Iron; Membrane; Metal-binding;

KW Cytochrome b.

KW Cytochrome b.

FT CHAIN 1 379

FT METAL 83 83 /FTID=PRO_0000060690.

FT METAL 97 97 Iron 1 (heme b562 axial ligand).

FT METAL 182 182 Iron 2 (heme b566 axial ligand).

FT METAL 196 196 Iron 1 (heme b562 axial ligand).

FT METAL 196 196 Iron 2 (heme b566 axial ligand).

SEQUENCE 379 AA; 42755 MW; 918399739658473 CRC64;

Query Match 13.7%; Score 10; DB 1; Length 379;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LLLTLLLLL 11
 DB 233 LLLTLLLLL 242

RESULT 8

O3UNC6_MOUSE

AC O3UNC6_MOUSE

DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.

DT 11-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Adult male gall bladder cDNA, RIKEN full-length enriched library,

DE clone:G630012H08 product:clone carrier family 27 (fatty acid

DE transporter), member 5, full insert sequence.

GN Name=SLC27A5;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Gall bladder;

RX PubMed=16141072; DOI=10.1126/science.1112014;

RA Carninci P., Katayama T., Katayama S., Gough J., Frith M.C., Maeda N.,

RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,

RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,

RA Davis M.J., Wilmink L.G., Aldrich V., Allen J.E.,

RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,

RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,

RA Chiu K.P., Choudhary V., Christofels A., Clutier D.R.,

RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

RA di Bernardo D., Down T., Engelstorfer P., Fagiolini M., Faulkner G.,

RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,

RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

RA Guetlich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,

RA Hall D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

RA Hatt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,

RA Liuni S., McMilliam S., Madan Babu M., Madera M., Marchionni L.,

RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Moris K.,

RA Mortagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,

RA Nilsson R., Nishiguchi S., Nishikawa S., Noji F., Ohara O.,

RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,

RA Petrowsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,

RA Roet B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,

RA Schombach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,

RA Shihata Y., Shimada H., Shimada K., Silva D., Sinclair B.,

RA Spelling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,

RA Tamoya K., Tan S.L., Tang S., Taylor W.S., Tegner J., Teichmann S.A.,

RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeig K.,

RA Yamanishi H., Zabarovsky E., Zhu B.T., Brusic V., Quackenbush J.,

RA Grimmond S.M., Teasdale R.D., Liu B.T., Brusic V., Quackenbush J.,

RA Wahlestedt C., Matlick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,

RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki Y., Arakawa T.,

RA Iida J., Imanura K., Itoh M., Kato T., Kawai H., Kawagashira N.,

RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Nimomiya N.,

RA Nishio T., Okada M., Plessey C., Shihata K., Shiraki T., Suzuki S.,

RA Tagami M., Waki K., Watanabe A., Okamura-Ohno Y., Suzuki H., Kawai J.,

RA Hayashizaki Y.;

RT "The transcriptional landscape of the mammalian genome.";

RL Science 309:1559-1563(2005).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Gall bladder;

RX PubMed=16141073; DOI=10.1126/science.1112009;

RG RIKEN Genome Exploration Research Group, and Genome Science Group

(Genome Network Core Team) and the FANTOM Consortium;

"Antisense Transcription in the Mammalian Transcriptome,"
Science 309:1564-1566(2005).

[4]

NCLECTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=gall bladder;
RX MEDLINE=22354683; PubMed=1246851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nkaido I., Osato N., Saito R., Suzuki H., Yamana K. I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotojori T.,
RA Baldairelli R., Hill D. P., Bult C., Hume D. A., Quackenbush J.,
RA Schirral L. M., Carninci A., Matsuda H., Batalov S., Beisel K. W.,
RA Blake J. A., Bradt D., Brusic V., Chothia C., Corbani L. E., Cousins S.,
RA Dalla E., Dragani T. A., Fletcher C. F., Forrest A., Frazer K. S.,
RA Gaasterland T., Gariboldi S., Gissi C., Godzik A., Gough J.,
RA Grumond S., Gustlicich S., Hirokawa N., Jackson I. J., Jarvis E. D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R. M., King B. L.,
RA Konagaya A., Kurochkin I. V., Lee Y., Lemhard B., Lyons P. A.,
RA Maglott D. R., Malraiz L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan M. J., Pereira G., Peesle G.,
RA Petrovsky N., Pillai R., Pontius J. U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J. C., Reed D. J., Reid J., Ring B. Z., Ringwald M.,
RA Sandelin A., Schneider C., Seiple C. A., Setou M., Shimada K.,
RA Salazar R., Takenaka Y., Taylor M. S., Teasdale R. D., Tomita M.,
RA Venardo R., Wagner L., Wahlstedt C., Wang Y., Waterman J., Wells C.,
RA Wilming L. G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozone-Kishikawa T., Kono H., Nakamura M., Sakakura N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Saeki D., Shibata K., Shingawa A.,
RA Yamashita A., Yoshino M., Waterson R., Lander E. S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs." ;
RN Nature 420:563-573(2002).

[5]

NCLECTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=gall bladder;
RX MEDLINE=1089660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinaga A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glisi C., King B. Z., Kochava H.,
RA Knehl P., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L. M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldairelli R., Barsh G.,
RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustlicich S., Hill D., Hofmann M., Hume D. A., Kamya M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momabets P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K. H., Weltz C., Whiteaker C., Wilting L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohitsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection." ;
RL Nature 409:685-690(2001).

[6]

NCLECTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=gall bladder;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes." ;
RL Genome Res. 10:1617-1630(2000).

[7]

NCLECTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=gall bladder;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Hizuna T., Tashiro H., Itoh M.,
RA Suno H., Ishii Y., Nakamura S., Kazuma M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwa K.,
RA Fujiwaka S., Inoue K., Togawa Y., Itawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771 (2000).
[8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Gall bladder;
RA Arkawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata K., Nakamura M., Ninomiya N.,
RA Nishiyori K., Nomura K., Ono M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Wataniki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC -I- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
family.

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CC EMBL, AK144301; BAE25821.1; -, mRNA.
DR MG1, X6147100; SIC27a5.
DR GO:GO:0005783; C:endoplasmic reticulum; TAS.
DR GO:GO:0003824; F:catalytic activity; RCA.
DR GO:GO:0004467; F:long-chain-fatty-acid-CoA ligase activity; TAS.
DR GO:GO:0001676; F:long-chain fatty acid metabolism; TAS.
DR GO:GO:0008152; P:metabolism; RCA.
DR InterPro: IPR000873; AMP-bind.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP BINDING: 1.
SQ SEQUENCE 418 AA; 45626 MW; CQ5738017FAFA7a1 CRC64;

Query Match 13.7%; Score 10; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 4 LTTLLLLLLL 13
|||||
Db 7 LTLLLTLTLL 16

RESULT 9
S27A5_MOUSE STANDARD; PRT; 689 AA.

ID S27A5_MOUSE
AC Q41DG0; O88694; Q91VD5;
DT 22-NOV-2005, integrated into UniProtKB/Swiss-Prot.
DT 22-NOV-2005, sequence version 2.
DI 07-MAR-2006, entry version 11.
DE Bile acyl-CoA synthetase (EC 6.2.1.7) (BACS) (Bile acid CoA ligase)
DE (BA-CoA ligase) (BAL) (Cholate--CoA ligase) (Very long chain acyl-CoA
DE synthetase-related protein) (VLACS-related) (VLACSR) (Fatty acid
DE transport protein 5) (PATP-5) (Soluble carrier family 27 member 5).
GN Name=SIC27a5; Synonyms=Acscb, Acsl16, Fatp5, VLacsr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=96308102; PubMed=9642112; DOI=10.1006/brcr.1998.8770;
RA Berger J., Tuppe C., Neumann H., Forss-Petter S.,
RT "A novel relative of the very-long-chain acyl-CoA synthetase and fatty
acid transporter protein genes with a distinct expression pattern.",
RL Biochem. Biophys. Res. Commun. 247:255-260(1998).
[2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC STRAIN=FVB/N; TISSUE=Saliivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheiner C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Batat F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelfano N.A., Peters G.J., Abmayron R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 28-689.
 RX MEDLINE=98337965; PubMed=9671728; DOI=10.1073/pnas.95.15.8625;
 RA Hirsch D., Stahl A., Lodish H.F.;
 RT "A family of fatty acid transporters conserved from mycobacterium to
 RT man.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX PubMed=11980911; DOI=10.1074/jbc.M203295200;
 RA Mihalik S.J., Steinberg S.J., Pei Z., Park G.,
 RA Heinzer A.K., DeRemont G., Wanders R.J., Creebs D.A., Smith K.D.,
 RA Watkins P.A.;
 RT "Participation of two members of the very long-chain acyl-CoA
 RT synthetase family in bile acid synthesis and recycling.";
 RL J. Biol. Chem. 277:24771-24779(2002).
 CC -1- FUNCTION: Acyl-CoA synthetase involved in bile acid metabolism.
 CC Proposed to catalyze the first step in the conjugation of C24 bile
 CC acids (cholestanoic) to glycine and taurine before excretion into
 CC bile canaliculi by activating them to their CoA thioesters. Seems
 CC to activate secondary bile acids entering the liver from the
 CC enterohepatic circulation (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + cholate + CoA = AMP + diphosphate +
 CC cholesteryl-CoA.
 CC -1- CATALYTIC ACTIVITY: ATP + (25R)-3-alpha,7-alpha,12-alpha-
 CC trihydroxy-5-beta-cholestan-26-oate + CoA = AMP + diphosphate +
 CC (25R)-3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum; endoplasmic reticulum
 CC membrane; multi-pass membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: In liver expressed in a periportal
 CC distribution.
 CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
 CC family.
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DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00455; AMP BINDING. 1.
 KW AMP-binding; Endoplasmic reticulum; Fatty acid metabolism; Ligase;
 KW Lipid metabolism; Membrane; Nucleotide-binding; Transmembrane.
 FT CHAIN 1 689
 FT
 FT TOPO_DOM 1 7
 FT TRANSMEM 8 28
 FT TRANSMEM 30 50
 FT TRANSMEM 55 75
 FT TOPO_DOM 76 689
 FT NP_BIND 292 303
 FT CONFLICT 88 88
 FT CONFLICT 408 408
 FT CONFLICT 568 568
 FT CONFLICT 688 688
 FT SEQUENCE 689 AA; 76203 MW; 1642B8C2CF04FAA3 CRC64;
 Query Match 13.7%; Score 10; DB 1; Length 689;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LTTLLLLLLL 13
 Db 7 LTTLLLLLLL 16
 RESULT 10
 ID Q5R588_PONPY PRELIMINARY; PRT; 39 AA.
 AC Q5R588;
 DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 21-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Hypothetical protein DKFZP459K2327.
 GN Name=DKFZP459K2327;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Pongo.
 OC NCBI_TaxID=96600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA TISSUE=Cortex;
 RG The German cDNA Consortium;
 RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL; CR660976; CAH3078.1; -; mRNA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000215; Prot_inh_serpin; 1.
 DR PANTHER; PTHR11461; Prot_inh_serpin; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 39 AA; 4116 MW; 1D7968215B1C4D12 CRC64;
 Query Match 12.3%; Score 9; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LTTLLLLLLL 11
 Db 7 LTTLLLLLLL 15
 RESULT 11
 ID Q4X6W7_PLACH PRELIMINARY; PRT; 52 AA.
 AC Q4X6W7;
 DT 05-JUN-2005, integrated into UniProtKB/TrEMBL.


```

DT 05-JUL-2005, sequence version 1.
DE 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN ORFNames=PC405632.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kataros F.C., Janse C.C., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; CAA01009385; CAA87359.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 52 AA; 5868 MW; 447EAA6E9ECE9802 CRC64;

Query Match 12.3%; Score 9; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 TTTTTTTT 14
Db 9 TTTTTTTT 17

RESULT 12
Q3R079.XYLFA PRELIMINARY; PRT; 61 AA.
ID Q3R079;
AC Q3R079;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein precursor.
GN ORFNames=XFASODRAF_0863;
OS Xylella fastidiosa Ann-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=155920;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ann-1;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hamon N., Iarant S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Xylella fastidiosa
RT Ann-1.";
RL Submitted (AUG-2005) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ann-1;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Xylella fastidiosa Ann-
RT 1.";
RL Submitted (AUG-2005) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ann-1;

```

```

RA DOE Joint Genome Institute;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ann-1;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hamon N., Iarant S., Pitluck S., Richardson P.;
RL Submitted (JUL-2005) to the EMBL/Genbank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAAW03000109; EAO30628.1; -; Genomic_DNA.
KW Hypothetical protein; Signal.
FT SIGNAL 1 47
SQ SEQUENCE 61 AA; 6846 MW; 3FB82714ECE41233 CRC64;

Query Match 12.3%; Score 9; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTTTTTTT 13
Db 8 TTTTTTTT 16

RESULT 13
Q8K4W3.MOUSE PRELIMINARY; PRT; 75 AA.
ID Q8K4W3.MOUSE
AC Q8K4W3;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Scotin (Fragment).
GN Name=Scotin;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ICR;Swiss;
RX MEDLINE=22131632; PubMed=12135983; DOI=10.1083/jcb.200203006;
RA Bourdon J.C., Renzing J., Robertson P.L., Fernandes K.N., Lane D.P.;
RT "Scotin, a novel p53-inducible proapoptotic protein located in the ER
RT and the nuclear membrane.";
RL J. Cell Biol. 158:235-246(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AF520701; AA074234.1; -; Genomic_DNA.
RC EMBL; AF520701; AA074234.1; JOINED; Genomic_DNA.
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CC -----
DR EMBL; AF520701; AA074234.1; -; Genomic_DNA.
DR EMBL; ENSMUSG00000025647; Mus musculus.
RN MGI; MGI:1915044; Scotin.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0005635; C:nuclear envelope; IDA.
DR GO; GO:0008632; P:apoptotic program; IDA.
DR GO; GO:0006917; P:induction of apoptosis; IDA.
FT NON TER 75
SQ SEQUENCE 75 AA; 8253 MW; DBB52F2072BE48AB CRC64;

Query Match 12.3%; Score 9; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTTTTTTT 13

```

Db 10 TLLLLLLL 18

RESULT 14

Q7NE75 GLOVI PRELIMINARY; PRT; 96 AA.
 AC Q7NE75_ GLOVI PRELIMINARY; PRT; 96 AA.
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Gal4005 protein.
 GN OrderedLocustNames=gsl4005;
 OS Gloeobacter violaceus.
 OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacteriales; Gloeobacter.
 OX NCBI_TaxID=33072;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RC STRAIN=PCC 7421;
 RX MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
 RA Nakamura Y., Kaneko T., Sato S., Miumro M., Miyashita H., Tsuchiya T.,
 RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
 RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpō S.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
 cyanobacterium that lacks thylakoids.";
 RL DNA Res. 10:137-145(2003).
 CC -----
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 CC -----
 DR EMBL: BA000045; BAC91946.1; -; Genomic DNA.
 DR BioCyc: GYIO251221:GSL4005-MONOMER; -.
 KW COMPLETE proteome.
 SQ SEQUENCE 96 AA; 11018 MW; 1C2FF96435784E92 CRC64;
 Query March 12.3%; Score 9; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred.No. 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LTTLLLLL 11
 Db 2 LTTLLLLL 10
 RESULT 15
 Q8MKI6_BOVIN PRELIMINARY; PRT; 99 AA.
 ID Q8MKI6_BOVIN PRELIMINARY; PRT; 99 AA.
 AC Q8MKI6;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE Prepro-orexin (Fragment).
 GN Name=BORX;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Watanabe K., Aso H., Sato T., Tahara K., Takano S., Yamaguchi T.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC -----
 DR EMBL: AB084625; BAB91446.1; -; mRNA.
 DR Ensembl: ENSBTAG00000000665; Bos taurus.
 DR GO: GO:0007631; P:feeding behavior; IEA.
 DR GO: GO:0007218; P:neuropeptide signaling pathway; IEA.
 DR InterPro: IPR001704; Orexin.
 DR PANTHER: PTHR15173; Orexin; 1.

DR Pfam: PF02072; Orexin; 1.
 DR PRINTS: PR01091; OREXINP.
 FT NON TER 99
 SQ SEQUENCE 99 AA; 10372 MW; 8F9F5E6B9EB8A5D CRC64;

Query Match 12.3%; Score 9; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred.No. 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TLLLLLLL 13
 Db 14 TLLLLLLL 22

Search completed: June 6, 2006, 21:14:29
 Job time : 296 secs

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OM protein - protein search, using sw model

Run on: June 6, 2006, 21:09:48 ; Search time 38 Seconds
(without alignments)
184.837 Million cell updates/sec

Title: US-10-063-534-30

Perfect score: 73

Sequence: 1 MLTLTLTLTLTLTKSGCLEW.....PAMTCQAOPRGEGKVDG 73

Scoring table: OLIGO

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1373

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database : PIR 801.*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	13.7	689	1 JMW0107	very-long-chain ac
2	9	12.3	208	2 B86014	probable enzyme yh
3	9	12.3	208	2 B91168	probable enzyme [l
4	9	12.3	208	2 S47687	hypothetical prote
5	9	12.3	381	2 S35940	class I histocompa
6	9	12.3	500	1 TTHUC1	complement C1 inh
7	9	12.3	537	2 T49162	hypothetical prote
8	9	12.3	1894	2 JG4960	plexin 1 precursor
9	8	11.0	53	2 S05486	alpha-amylase (EC
10	8	11.0	77	2 A03982	p15E protein - sim
11	8	11.0	82	2 JQ1181	outer envelope mem
12	8	11.0	101	2 B28414	growth-regulated p
13	8	11.0	112	2 A60111	sporozoite antigen
14	8	11.0	131	2 PQ0059	T-cell receptor be
15	8	11.0	133	2 JG2022	secretin precursor
16	8	11.0	133	2 S57038	probable membrane
17	8	11.0	134	2 A40959	secretin precursor
18	8	11.0	135	2 C82176	hypothetical prote
19	8	11.0	144	2 T18867	hypothetical prote
20	8	11.0	171	2 S19502	hypothetical prote
21	8	11.0	182	2 J18063	neuromedin U precu
22	8	11.0	182	2 JG7236	receptor-activit
23	8	11.0	185	2 A49957	CD45-associated 30
24	8	11.0	185	2 I40490	hypothetical prote
25	8	11.0	189	2 JG7262	receptor activity
26	8	11.0	197	2 S51372	membrane protein L
27	8	11.0	201	2 J18850	LEKK-4 - human
28	8	11.0	205	2 S37804	hypothetical prote
29	8	11.0	206	2 S18250	collagen alpha 1(I

30	8	11.0	206	2 A55412	lymphocyte phospho
31	8	11.0	208	2 T06492	ribosomal protein
32	8	11.0	208	2 AC0091	probable membrane
33	8	11.0	208	2 AC0465	probable membrane
34	8	11.0	220	2 S43291	FLT3/FLK2 ligand (
35	8	11.0	220	2 I58343	FLT3 ligand isofor
36	8	11.0	231	2 A49265	FLT3/FLK-2 ligand
37	8	11.0	244	2 S18948	centrocyclin precu
38	8	11.0	245	1 C1HUOC	complement subcomp
39	8	11.0	249	1 A35842	chymase (EC 3.4.21
40	8	11.0	259	2 A71537	probable n-acetyl
41	8	11.0	263	2 S57346	interleukin 15 rec
42	8	11.0	285	2 JC5639	1-acetylglucosyl-3-p
43	8	11.0	291	2 B60131	homeocytic protein X
44	8	11.0	304	2 T02679	probable RNA-bind
45	8	11.0	318	2 I59301	bone marrow stroma

ALIGNMENTS

RESULT 1

JM0107 very-long-chain acyl-CoA synthetase related protein - mouse

N:Alternate names: VLACSR

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: JM0107

R:Berger, J.; Truppe, C.; Neumann, H.; Forss-Petter, S.

Biochem. Biophys. Res. Commun. 247, 255-260, 1998

A:Title: A novel relative of the very-long-chain acyl-CoA synthetase and fatty acid trans

A:Reference number: JM0107; MUID:98308102; PMID:9642112

A:Accession: JM0107

A:Molecule type: mRNA

A:Residues: 1-689 <BER>

A:Cross-references: UNIPROT:Q91VD5; UNIPARC:UPI0000174C70; GB:AJ223959

A:Experimental source: liver

C:Comment: This protein likely functions as a plasma membrane transporter of long chain f

cids.

C:Superfamily: Mycobacterium tuberculosis probable fadD6 protein; acetate-CoA ligase hom

F;169-647/Domains: acetate-CoA ligase homology <ACL>

Query Match 13.7%; Score 10; DB 1; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTLTLTLTLTL 13
|||||
Db 7 LTLTLTLTLTL 16

RESULT 2

B86014 probable enzyme yhhn [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: B86014

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,

Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B86014

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-208 <STO>

A:Cross-references: UNIPROT:P37616; UNIPARC:UPI0000165965; GB:AE005174; NID:g12518127; P

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: yhhn

C:Superfamily: Escherichia coli hypothetical protein c208

Query Match 12.3%; Score 9; DB 2; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LTLTLTL 12
| | | | |
Db 33 LTLTLTL 41

RESULT 3

E91168
probable enzyme [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: E91168
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: E91168
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-208 <HAV>
A/Cross-references: UNIPROT:P37616; UNIPARC:UPI000013B251; GB:BA000007; PIDN:BA037740.1;
A/Experimental source: strain O157:H7, substrain RMD 0509952
C/Genetics:
A/Gene: EC64317
C/Superfamily: Escherichia coli hypothetical protein o208

Query Match 12.3%; Score 9; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LTLTLTL 12
| | | | |
Db 33 LTLTLTL 41

RESULT 4

S47687
hypothetical protein o208 - Escherichia coli (strain K-12)
N/Alternate names: hypothetical protein B3468
C/Species: Escherichia coli
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
C/Accession: S47687; G65143
R/Punkett, G.
submitted to the EMBL Data Library, March 1994
A/Reference number: S47687
A/Accession: S47687
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-208 <PLU>
A/Cross-references: UNIPROT:P37616; UNIPARC:UPI000013B251; EMBL:U00039; NID:g466582; PID
R/Baltner, F.R.; Punkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: G65143
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-208 <BLAT>
A/Cross-references: UNIPARC:UPI000013B251; GB:AE004422; GB:U00096; NID:g1789868; PIDN:AA
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: Escherichia coli hypothetical protein o208

Query Match 12.3%; Score 9; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LTLTLTL 12
| | | | |
Db 33 LTLTLTL 41

RESULT 5

S35940
class I histocompatibility antigen DLA-6.7B - dog
C/Species: Canis lupus familiaris (dog)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S35940
R/Burnett, R.C.
submitted to the EMBL Data Library, August 1993
A/Description: Molecular analysis of a canine MHC class Ib gene, DLA-6.7B.
A/Reference number: S35940
A/Accession: S35940
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-381 <BUR>
A/Cross-references: UNIPROT:Q30428; UNIPARC:UPI0000089557; EMBL:Z25418; NID:g396224; PID
C/Genetics:
A/Introns: 30/1; 121/1; 213/1; 305/1; 343/1; 359/1; 373/1
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
F/226-291/Domain: immunoglobulin homology <IMM>

Query Match 12.3%; Score 9; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TLTLTLTL 13
| | | | |
Db 8 TLTLTLTL 16

RESULT 6

ITRUC1
complement C1 inhibitor precursor [validated] - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Oct-2004
C/Accession: S15386; S00403; A38781; B38781; A24161; A38782; S03370; A34847; S15084; A24;
R/Carter, P.E.; Duponchel, C.; Toel, M.; Fochergill, J.E.
Eur. J. Biochem. 197, 301-308, 1991
A/Title: Complete nucleotide sequence of the gene for human C1 inhibitor with an unusual
A/Reference number: S15386; MUID:91224119; PMID:2026152
A/Accession: S15386
A/Molecule type: DNA
A/Residues: 1-500 <CA2>
A/Cross-references: UNIPROT:P05155; UNIPARC:UPI00000123F; EMBL:X54486; NID:g29534; PIDN
R/Carter, P.E.; Dunbar, B.; Fochergill, J.E.
Eur. J. Biochem. 173, 163-169, 1988
A/Title: Genomic and cDNA cloning of the human C1 inhibitor. Intron-exon junctions and c
A/Reference number: S00403; MUID:88185313; PMID:3267220
A/Accession: S00403
A/Molecule type: DNA
A/Residues: 1-500 <CAR>
A/Cross-references: UNIPARC:UPI00000123F; EMBL:X07427; NID:g29520; PIDN:CAA30314.1; PID
A/Accession: A38781
A/Residues: 178-500 <CA3>
A/Cross-references: UNIPARC:UPI000016A617; GB:X07577; NID:g29536; PIDN:CAA30469.1; PID:g3
A/Accession: B38781
A/Molecule type: protein
A/Residues: 173-237, 'X', 239-252, 'X', 254, 'X', 256-264, 'X', 266-268, 277-286, 330-333, 335-340, '
A/Cross-references: UNIPARC:UPI000004CC4B; UNIPARC:UPI0000042395; UNIPARC:UPI00001731BA;
1BF
R/Boek, S.C.; Skriver, K.; Nielsen, E.; Thogersen, H.C.; Wieman, B.; Donaldson, V.H.; Edý
Biochemistry 25, 4292-4301, 1986
A/Title: Human C1 inhibitor: primary structure, cDNA cloning, and chromosomal localization
A/Reference number: A24161; MUID:87000544; PMID:3756141
A/Accession: A24161
A/Molecule type: mRNA
A/Residues: 1-186, 'O', 188-500 <BOC>
A/Cross-references: UNIPARC:UPI0000145144; EMBL:M13656; NID:g179620; PIDN:AA059387.1; PII
A/Accession: A38782
A/Molecule type: protein
A/Residues: 23-500 <BO2>

A:Cross-references: UNIPARC:UPI00001731C0
A:Note: 480-Met was also found
R:Rauth, G.; Schumacher, G.; Buckel, P.; Mueller-Esterl, W.
Protein Seq. Data Anal. 1, 251-257, 1988
A:Title: Molecular cloning of the CDNA coding for human C1(-) inhibitor.
A:Reference number: S03370; MUID:88276848; PMID:3393514
A:Accession: S03370
A:Molecule type: mRNA
A:Residues: 'PPVO', 6-479, 'M', 481-500 <RAU>
A:Cross-references: UNIPARC:UPI00001731C1
R:Stoppa-Lyonnet, D.; Carter, P.E.; Meo, T.; Tosi, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 1551-1555, 1990
A:Title: Clusters of intragenic Alu repeats predispose the human C1 inhibitor locus to a
A:Reference number: A34847; MUID:90160364; PMID:2154751
A:Accession: A34847
A:Molecule type: DNA
A:Residues: 33-228 <STO>
A:Cross-references: UNIPARC:UPI00001731C2; GB:M30688
R:Que, B.G.
Submitted to the EMBL Data Library, November 1986
A:Reference number: S15084
A:Accession: S15084
A:Molecule type: mRNA
A:Residues: 1-305, 'R', 307-500 <QUE>
A:Cross-references: UNIPARC:UPI000016A615; EMBL:M13690; NID:g179618; PIDN:AAA5613.1; PI
R:Que, B.G.; Petrá, P.H.
Biochem. Biophys. Res. Commun. 137, 620-625, 1986
A:Title: Isolation and analysis of a cDNA coding for human C1 inhibitor.
A:Reference number: A24258; MUID:86268965; PMID:3488058
A:Accession: A24258
A:Molecule type: mRNA
A:Residues: 187, 'K', 189-408, 413-500 <OU2>
A:Cross-references: UNIPARC:UPI00001731C3; EMBL:M13690
R:Tosi, M.; Duponchel, C.; Bourgarel, P.; Colomb, M.; Meo, T.
Gene 42, 265-272, 1986
A:Title: Molecular cloning of human C1 inhibitor: sequence homologies with alpha(1)-anti
A:Reference number: S15529; MUID:86276001; PMID:3089875
A:Accession: S15529
A:Molecule type: mRNA
A:Residues: 213-500 <TOS>
A:Cross-references: UNIPARC:UPI000016A614; EMBL:M14036; NID:g179616; PIDN:AAA51848.1; PI
R:Davis III, A.E.; Whitehead, A.S.; Harrison, R.A.; Daughnals, A.; Bryns, G.A.P.; Cicaz
Proc. Natl. Acad. Sci. U.S.A. 83, 3161-3165, 1986
A:Title: Human inhibitor of the first component of complement, C1: characterization of c
A:Reference number: A23936; MUID:86205856; PMID:3458172
A:Accession: A23936
A:Molecule type: mRNA
A:Residues: 241-314, 'QLOQLSY', 321, 'M', 323-331, 'L', 333-369, 'TGTGSO', 376-416, 'V', 418-438, '
A:Cross-references: UNIPARC:UPI00001731C4; EMBL:M13203
A:Note: the authors translated the codon CTG for residue 332 as Val
A:Accession: A38783
A:Molecule type: protein
A:Residues: 23-24, 'X', 26-33, 54-62, 'XL', 168-178, 'X', 180-186, 'NAEAX', 192, 'X', 194, 326-351, '
A:Cross-references: UNIPARC:UPI00001731C5; UNIPARC:UPI00001731C6; UNIPARC:UPI00001731C7;
R:Harrison, R.A.
Biochemistry 22, 5001-5007, 1983
A:Title: Human C1 inhibitor: improved isolation and preliminary structural characterizati
A:Reference number: A05286; MUID:84053355; PMID:6416294
A:Accession: S15085
A:Molecule type: protein
A:Residues: 23-24, 'X', 26-47, 'X', 48-62 <HAR>
A:Cross-references: UNIPARC:UPI00001731CB
R:Salvesen, G.S.; Caranese, J.J.; Kress, L.F.; Travis, J.
J. Biol. Chem. 260, 2432-2436, 1985
A:Title: Primary structure of the reactive site of human C1-inhibitor.
A:Reference number: S15086; MUID:85130986; PMID:3919001
A:Accession: S15086
A:Molecule type: protein
A:Residues: 'I', 61-62, 'XX', 65-68, 464-475 <SAL>
A:Cross-references: UNIPARC:UPI00001731CC; UNIPARC:UPI00001731CD
R:Parad, R.B.; Krimer, U.; Strunk, R.C.; Rosen, F.S.; Davis III, A.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 6786-6790, 1990
A:Title: Dysfunctional C1 inhibitor Ta: deletion of Lys-251 results in acquisition of an

A:Reference number: A36053; MUID:90370868; PMID:2118657
A:Accession: A36053
A:Molecule type: protein
A:Residues: 266-282 <PAR>
A:Cross-references: UNIPARC:UPI00001731CE
A:Note: Lys-251 was deleted in protein isolated from a patient with type II hereditary a
C:Comment: This protein inhibits the serine proteinase activity in complement factors C1
C:Genetics: Defects in this protein result in hereditary angioneurotic edema. In type I d
A:Gene: GDB:CLNH
A:Cross-references: GDB:119041; OMIM:106100
A:Map position: 11q12.1-11q13.1
A:Introns: 17/3; 184/1; 229/1; 297/1; 343/3; 417/1
C:Superfamily: serpin
C:Keywords: glycoprotein; serine proteinase inhibitor; tandem repeat
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-500/Product: complement C1 inhibitor #status experimental <MAT>
F:23-119/Domain: glycosylated #status predicted <GLC>
F:65-119/Region: 4-residue repeats
F:120-500/Domain: inhibitory #status predicted <INH>
F:25-69, 81, 238, 253, 352/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:48, 71, 83, 88, 92, 96/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:64/Binding site: carbohydrate (Ser) (covalent) #status experimental
F:72, 99, 106, 107, 111, 115, 118, 119/Binding site: carbohydrate (Thr) (covalent) #status pred.
F:123-428, 130-205/Disulfide bonds: #status experimental
F:466/Inhibitory site: Arg (complement C1) #status experimental
Query Match 12.3%; Score 9; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 3 LTLTLTLTL 11
Db 7 LTLTLTLTL 15
RESULT 7
T49162
hypotheical protein T20N10.140 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence, revision 02-Jun-2000 #text, change 09-Jul-2004
C:Accession: T49162
R:DiAngelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25017
A:Accession: T49162
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-537 <DNAN>
A:Cross-references: UNIPROT:Q9LX53; UNIPARC:UPI000009F3C5; EMBL:AL553032; GSPDB:GN00061;
C:Genetics:
A:Experimental source: cultivar Columbia; BAC clone T20N10
A:Gene: ATSP:T20N10.140
A:Map position: 3
A:Introns: 80/1; 94/3; 150/3; 342/3; 443/3
Query Match 12.3%; Score 9; DB 2; Length 537;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 5 TLLTLTLTL 13
Db 45 TLLTLTLTL 53
RESULT 8
JC4980
plexin 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence, revision 31-Dec-1996 #text, change 09-Jul-2004
C:Accession: JC4980
R:Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, I
Biochem. Biophys. Res. Commun. 226, 524-529, 1996

A/Title: Identification of a neuronal cell surface molecule, plexin, in mice.
 A/Reference number: JC4980; MUID:96400291; PMID:8806667
 A/Accession: JC4980
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-1894 <FAM>
 A/Cross-references: UNIPROT:P70206; UNIPARC:UPI00000233AE; DBJ:D86948; NID:g1665756; PI
 A/Experimental source: brain
 C/Comment: This protein is a membrane protein, and plays a role in neuronal cell contact
 sence of calcium ions.
 C/Keywords: duplication; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:513-561,659-704,807-859/Region: cysteine-rich
 F:1238-1264/Domain: transmembrane #status predicted <TMM>
 F:1266-1268/Region: hydrophilic

Query Match 12.3%; Score 9; DB 2; Length 1894;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 LLLLLLLL 13
 |||||
 Db 10 LLLLLLLL 18

RESULT 9
 S05486
 alpha-amylase (EC 3.2.1.1) 2.34 precursor - wheat (fragment)
 C/Species: Triticum aestivum (common wheat)
 C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004
 C/Accession: S05486
 R:Huttlly, A.K.; Martienssen, R.A.; Baulcombe, D.C.
 Mol. Gen. Genet. 214, 232-240, 1988
 A/Title: Sequence heterogeneity and differential expression of the alpha--Amy-2 gene fan
 A/Reference number: S05486; MUID:83181522; PMID:2467183
 A/Accession: S05486
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-53 <HUT>
 A/Cross-references: UNIPROT:P11784; UNIPARC:UPI00000A6FDC; EMBL:X13578; NID:g21662; PIDN
 C/Genetics:
 A/Gene: amy2
 A/Map position: 7D
 A/Intons: 32/3
 C/Function:
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amylase; plant type; alpha-amylase core homology
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 11.0%; Score 8; DB 2; Length 53;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLLL 13
 |||||
 Db 12 LLLLLLLL 19

RESULT 10
 A03982
 p15E protein - simian sarcoma virus (fragment)
 C/Species: simian sarcoma virus
 C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 C/Accession: A03982
 R/Devare, S.G.; Reddy, E.P.; Law, J.D.; Robbins, K.C.; Aaronson, S.A.
 Proc. Natl. Acad. Sci. U.S.A. 80, 731-735, 1983
 A/Title: Nucleotide sequence of the simian sarcoma virus genome: demonstration that its
 A/Reference number: A03982; MUID:83144004; PMID:6298772
 A/Accession: A03982
 A/Molecule type: genomic RNA
 A/Residues: 1-77 <DEV>
 A/Cross-references: UNIPROT:P03384; UNIPARC:UPI000012A05A; GB:V01201; GB:J02394; GB:J023

C/Genetics:
 A/Gene: env
 C/Superfamily: type C retrovirus env polyprotein

Query Match 11.0%; Score 8; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLLL 13
 |||||
 Db 31 LLLLLLLL 38

RESULT 11
 JQ1181
 outer envelope membrane 14K protein, chloroplast - garden pea
 C/Species: Pisum sativum (garden pea)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 19-Jan-1996
 C/Accession: JQ1181
 R:Li, H.M.; Moore, T.; Keegstra, K.
 Plant Cell 3, 709-717, 1991
 A/Title: Targeting of proteins to the outer envelope membrane uses a different pathway ct
 A/Reference number: JQ1181; MUID:93044506; PMID:1641725
 A/Accession: JQ1181
 A/Molecule type: mRNA
 A/Residues: 1-82 <LIH>
 A/Cross-references: UNIPARC:UPI000017B068; GB:M69105
 A/Experimental source: leaf, cv. Perfection
 C/Keywords: chloroplast; membrane protein

Query Match 11.0%; Score 8; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LLLLLLLK 14
 |||||
 Db 48 LLLLLLLK 55

RESULT 12
 B28414
 growth-regulated protein precursor - Chinese hamster
 C/Species: Crictetus griseus (Chinese hamster)
 C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C/Accession: B28414
 R:Antosiewicz, A.; Bardwell, L.; Sager, R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7168-7192, 1987
 A/Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese h
 A/Reference number: A94184; MUID:88041072; PMID:2890161
 A/Accession: B28414
 A/Molecule type: mRNA
 A/Residues: 1-101 <ANI>
 A/Cross-references: UNIPROT:P09340; UNIPARC:UPI000012BAF7; GB:J03560; NID:g191088; PIDN:/
 A/Note: the authors translated the codon CAG for residue 52 as Glu
 C/Superfamily: beta-chromoglobulin
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-101/Product: growth-regulated protein #status predicted <MAT>

Query Match 11.0%; Score 8; DB 2; Length 101;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 LLLLLLLL 13
 |||||
 Db 13 LLLLLLLL 20

RESULT 13
 A60111
 sporozoite antigen - Eimeria tenella (fragment)
 C/Species: Eimeria tenella
 C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 17-Jul-1994
 C/Accession: A60111

R/Miller, G.A.; Bhogal, B.S.; McCandliss, R.; Strausberg, R.L.; Jesse, E.J.; Anderson, Infect. Immun. 57, 2014-2020, 1989
A/Title: Characterization and vaccine potential of a novel recombinant coccidial antigen
A/Reference number: A60111; MUID:89277516; PMID:2659532
A/Accession: A60111
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-112 <MIL>
A/Cross-references: UNIPARC:UPI0000142143

Query Match 11.0%; Score 8; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 LLLLLLL 13
| | | | |
Db 1 LLLLLLL 8

RESULT 14

PQ0059
T-cell receptor beta chain (RTB93) - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-May-1997
C/Accession: PQ0059
R/Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID May 1990
A/Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A/Reference number: U00472
A/Accession: PQ0059
A/Molecule type: mRNA
A/Residues: 1-131 <ACC>
A/Cross-references: UNIPARC:UPI000011D083
A/Experimental source: T cell
C/Genetics:
A/Gene: BTB93
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 11.0%; Score 8; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LLLLLLL 11
| | | | |
Db 2 LLLLLLL 9

RESULT 15

JC2202
secretin precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C/Accession: JC2202; S34214
R/Lan, M.S.; Kajiyama, W.; Donadel, G.; Lu, J.; Notkins, A.L.
Biochem. Biophys. Res. Commun. 200, 1066-1071, 1994
A/Title: cDNA sequence and genomic organization of mouse secretin.
A/Reference number: JC2202; MUID:9423495; PMID:8179583
A/Accession: JC2202
A/Molecule type: mRNA
A/Residues: 1-133 <LAN>
A/Cross-references: UNIPROT:008535; UNIPARC:UPI0000026321; EMBL:X73580; NID:G313710; PID
C/Comment: This protein regulates the secretion of pancreatic juices and stimulates insu
C/Superfamily: glucagon
C/Keywords: amidated carboxyl end; duplication; hormone; secretagogue
F/1-27/Domain: signal sequence #status predicted <SIG>
F/28-133/Product: prosecretin #status predicted <PRO>
F/32-58/Product: secretin #status predicted <MAT>
F/58/Modified site: amidated carboxyl end (Val) (amide in mature form from following gly

Query Match 11.0%; Score 8; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 LLLLLLL 13
| | | | |
Db 10 LLLLLLL 17

Search completed: June 6, 2006, 21:15:12
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: June 6, 2006, 21:51:09 / Search time 16 Seconds
(without alignments)
52.766 Million cell updates/sec

Title: US-10-063-534-30

Perfect score: 386
Sequence: 1 MLTLTLTLTLKSGCLEW.....PAMTCQAQPRGEGKVDG 73

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB pep:*
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	386	100.0	73	US-11-101-316-30	Sequence 30, Appl
2	63	16.3	124	US-10-953-349-14153	Sequence 14153, A
3	62.5	16.2	86	US-10-953-349-30624	Sequence 30624, A
4	59	15.3	91	US-10-953-349-14154	Sequence 14154, A
5	59	15.3	142	US-10-511-937-2432	Sequence 2432, Ap
6	59	15.3	468	US-10-953-349-10909	Sequence 10909, A
7	59	15.3	463	US-10-953-349-10908	Sequence 10908, A
8	59	15.3	503	US-10-953-349-10907	Sequence 10907, A
9	58.5	15.2	155	US-10-953-349-35222	Sequence 35222, A
10	58	15.0	432	US-10-196-749-74	Sequence 74, Appl
11	57.5	14.9	166	US-10-953-349-35817	Sequence 35817, A
12	57.5	14.9	215	US-10-953-349-35815	Sequence 35815, A
13	56	14.5	208	US-10-953-349-15677	Sequence 15677, A
14	56	14.5	864	US-11-312-797-2	Sequence 2, Appl
15	55	14.2	85	US-10-953-349-27987	Sequence 27987, A
16	55	14.2	547	US-11-293-697-2751	Sequence 2751, Ap
17	54	14.0	456	US-10-953-349-38513	Sequence 38513, A
18	53.5	13.9	338	US-11-106-014-12	Sequence 12, Appl
19	53.5	13.9	363	US-10-511-937-2530	Sequence 2530, Ap
20	53.5	13.9	1058	US-11-251-673-3	Sequence 3, Appl
21	53	13.7	193	US-10-953-349-9405	Sequence 9405, Ap
22	53	13.7	210	US-10-953-349-9404	Sequence 9404, Ap
23	53	13.7	882	US-10-196-749-574	Sequence 574, App
24	53	13.7	1038	US-10-511-937-2443	Sequence 2443, Ap
25	52.5	13.6	269	US-10-511-455-19	Sequence 19, Appl

26	52.5	13.6	308	US-10-511-455-23	Sequence 23, Appl
27	52.5	13.6	308	US-10-511-455-25	Sequence 25, Appl
28	52.5	13.6	314	US-10-511-455-21	Sequence 21, Appl
29	52.5	13.6	347	US-10-511-455-17	Sequence 17, Appl
30	52.5	13.6	347	US-10-511-455-28	Sequence 28, Appl
31	52.5	13.6	348	US-10-505-928-399	Sequence 399, App
32	52.5	13.6	348	US-10-511-455-15	Sequence 15, Appl
33	52.5	13.6	348	US-10-511-455-27	Sequence 27, Appl
34	52.5	13.6	350	US-10-511-455-29	Sequence 29, Appl
35	52.5	13.6	410	US-10-953-349-20599	Sequence 20599, A
36	52.5	13.6	430	US-10-953-349-20598	Sequence 20598, A
37	52.5	13.6	451	US-10-953-349-20597	Sequence 20597, A
38	52.5	13.6	791	US-11-318-939-6	Sequence 6, Appl
39	52	13.5	120	US-10-953-349-23921	Sequence 23921, A
40	52	13.5	144	US-10-953-349-40121	Sequence 40121, A
41	52	13.5	152	US-10-953-349-23920	Sequence 23920, A
42	52	13.5	157	US-10-953-349-23919	Sequence 23919, A
43	52	13.5	283	US-10-953-349-22187	Sequence 22187, A
44	52	13.5	531	US-10-953-349-22037	Sequence 22037, A
45	52	13.5	533	US-10-953-349-22036	Sequence 22036, A

ALIGNMENTS

RESULT 1
US-11-101-316-30
Sequence 30, Application US/1101316
Publication No. US20060099657A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
FILE REFERENCE: P3230R1C17C1
CURRENT APPLICATION NUMBER: US/11/101.316
CURRENT FILING DATE: 2005-04-06
PRIOR APPLICATION NUMBER: 10/063526
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 09/380137
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 30
LENGTH: 73
TYPE: PRT
ORGANISM: Homo Sapien
US-11-101-316-30
Query Match 100.0%; Score 386; DB 7; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.8e-40;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLTLTLTLTLKSGCLEWLVGAKVSSATDAPRIDMAFPSPFLCLPHRAMTCQ 60
DB 1 MLTLTLTLTLKSGCLEWLVGAKVSSATDAPRIDMAFPSPFLCLPHRAMTCQ 60
QY 61 AOPRGEKVDG 73
DB 61 AOPRGEKVDG 73
RESULT 2

US-10-953-349-14153
; Sequence 14153, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14153
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-14153

Query Match 16.3%; Score 63; DB 6; Length 124;
Best Local Similarity 28.0%; Pred. No. 0.49;
Matches 26; Conservative 11; Mismatches 32; Indels 24; Gaps 4;

QY 2 LLTLLTLL-----LLKQSC-----LEWGLVGAQKVSATDAPTRDW 39
||| ||| : : : : :
Db 9 ILTLTLVHHEKRFSCFFEFVWVSCFEDDKTNVKAAGKVGAGAGYGALERMF 68
||| : : : : :
QY 40 AFPPSFCLLPHRPMTCSQAQPRGGEKVD 72
||| : : : : :
Db 69 LSFPTT-KTYFPHFD-LSHSAQVKGHGKQVAD 99
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RESULT 3
US-10-953-349-30624
; Sequence 30624, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30624
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30624

Query Match 16.2%; Score 62.5; DB 6; Length 86;
Best Local Similarity 31.9%; Pred. No. 0.38;
Matches 23; Conservative 3; Mismatches 29; Indels 17; Gaps 3;

QY 16 SCLEWGLVGAQKVSATDAPTRDW---AFF-----PPSFCLLPHRPMTCSQAQPRGGEKVD 58
||| ||| : : : : :
Db 15 SCSSTSPAGIQAAPASAGRLPPAAMCPAVFGSPSAPBPAPCGGARRPQCGNSLGHGNGC 74
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QY 59 SQAQPRGGEKVD 70
||| ||| : : : : :
Db 75 GGASPPAGEGERV 86
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RESULT 4
US-10-953-349-14154
; Sequence 14154, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14154
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-14154

Query Match 15.3%; Score 59; DB 6; Length 91;
Best Local Similarity 34.0%; Pred. No. 1.1;
Matches 18; Conservative 7; Mismatches 26; Indels 2; Gaps 2;

QY 20 WGLVGAQKVSATDAPTRDWAFFPPSFCLLPHRPMTCSQAQPRGGEKVD 72
||| ||| : : : : :
Db 16 WGVKGAHAGEYGALERMFLSFPTT-KTYFPHFD-LSHSAQVKGHGKQVAD 66
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RESULT 5
US-10-511-937-2432
; Sequence 2432, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2432
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2432

Query Match 15.3%; Score 59; DB 6; Length 142;
Best Local Similarity 34.0%; Pred. No. 1.7;
Matches 18; Conservative 7; Mismatches 26; Indels 2; Gaps 2;

QY 20 WGLVGAQKVSATDAPTRDWAFFPPSFCLLPHRPMTCSQAQPRGGEKVD 72
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Db 15 WGVKGAHAGEYGALERMFLSFPTT-KTYFPHFD-LSHSAQVKGHGKQVAD 65
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RESULT 6
US-10-953-349-10909
; Sequence 10909, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10909

LENGTH: 468
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-10908

Query Match 15.3%; Score 59; DB 6; Length 468;
Best Local Similarity 34.0%; Pred. No. 6.1;
Matches 18; Conservative 7; Mismatches 26; Indels 2; Gaps 2;
QY 20 WGLVGAQKVSATDAPTRDWAFFPPSFLCLPHRPAMTCSQAQPRGEGEKYGD 72
DB 393 WGVKGAHAGEYGABALERMFLSFPTT-KTYPPHFD-LSHSGAQQKGGKXVAD 443

RESULT 7
US-10-953-349-10908
Sequence 10908, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953.349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10908
LENGTH: 469
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-10908

Query Match 15.3%; Score 59; DB 6; Length 469;
Best Local Similarity 34.0%; Pred. No. 6.1;
Matches 18; Conservative 7; Mismatches 26; Indels 2; Gaps 2;
QY 20 WGLVGAQKVSATDAPTRDWAFFPPSFLCLPHRPAMTCSQAQPRGEGEKYGD 72
DB 394 WGVKGAHAGEYGABALERMFLSFPTT-KTYPPHFD-LSHSGAQQKGGKXVAD 444

RESULT 8
US-10-953-349-10907
Sequence 10907, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953.349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10907
LENGTH: 503
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-10907

Query Match 15.3%; Score 59; DB 6; Length 503;
Best Local Similarity 34.0%; Pred. No. 6.6;
Matches 18; Conservative 7; Mismatches 26; Indels 2; Gaps 2;
QY 20 WGLVGAQKVSATDAPTRDWAFFPPSFLCLPHRPAMTCSQAQPRGEGEKYGD 72
DB 428 WGVKGAHAGEYGABALERMFLSFPTT-KTYPPHFD-LSHSGAQQKGGKXVAD 478

RESULT 9
US-10-953-349-35222
Sequence 35222, Application US/10953349

Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953.349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35222
LENGTH: 155
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LOCATION: (48)..(48)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (81)..(81)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-35222

Query Match 15.2%; Score 58.5; DB 6; Length 155;
Best Local Similarity 35.0%; Pred. No. 2.2;
Matches 14; Conservative 5; Mismatches 16; Indels 5; Gaps 2;
QY 30 SATDAPTRDWAFFP---PSFLCLLP-HRPAMTCSQAQPR 64
DB 103 SPSSSPTRSWFWFAGTCSAFCCSLRLEGSAACPSSTPR 142

RESULT 10
US-10-136-749-74
Sequence 74, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430RIC340
CURRENT APPLICATION NUMBER: US/10/196.749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544

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; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 74
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-74

Query Match      15.0%; Score 58; DB 6; Length 432;
Best Local Similarity 43.8%; Pred. No. 7.4;
Matches 14; Conservative 3; Mismatches 15; Indels 0; Gaps 0;

Dy      4 LTTLLLLLLKSGSCLWGLVQAQVSSATDAP 35
Db      18 LTTALLLLLLGGGGKRGARQAQEAALAAADGP 49

RESULT 11
US-10-953-349-35817
; Sequence 35817, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35817
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (137)..(137)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-35817

Query Match      14.9%; Score 57.5; DB 6; Length 166;
Best Local Similarity 28.1%; Pred. No. 3.1;
Matches 27; Conservative 6; Mismatches 24; Indels 39; Gaps 5;

Dy      4 LTTLLLLLLKSGSCLWGLV-----AQVSSATDAP1-----RDW 39
Db      22 LTTLLPRLLLASPSLPSAAAPSPPTVATGQAASDASDAPPPRPAQCHRRHRHWH 81

Dy      40 AFFFFSFLCLPHRPAMTCSQAQPRGE---GEKVG 71
Db      82 KHRPPP-----PHPP-----PPPRRRRLNGERLIG 106

RESULT 12
US-10-953-349-35815
; Sequence 35815, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35815
; LENGTH: 215
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; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (60)..(60)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (186)..(186)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-35815

Query Match      14.9%; Score 57.5; DB 6; Length 215;
Best Local Similarity 28.1%; Pred. No. 4.1;
Matches 27; Conservative 6; Mismatches 24; Indels 39; Gaps 5;

Dy      4 LTTLLLLLLKSGSCLWGLV-----AQVSSATDAP1-----RDW 39
Db      71 LTTLLPRLLLASPSLPSAAAPSPPTVATGQAASDASDAPPPRPAQCHRRHRHWH 130

Dy      40 AFFFFSFLCLPHRPAMTCSQAQPRGE---GEKVG 71
Db      131 KHRPPP-----PHPP-----PPPRRRRLNGERLIG 155

RESULT 13
US-10-953-349-15677
; Sequence 15677, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15677
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15677

Query Match      14.5%; Score 56; DB 6; Length 208;
Best Local Similarity 56.5%; Pred. No. 6;
Matches 13; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Dy      1 MLTTLLLLLLKSGSCLWGLV 23
Db      85 LTTLLLLQLLLLRPLLLQWQL 107

RESULT 14
US-11-312-797-2
; Sequence 2, Application US/11312797
; Publication NO. US20060100151A1
; GENERAL INFORMATION:
; APPLICANT: Trout, Anthony
; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Apple PowerMacintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
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? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/11/312,797
? FILING DATE: 20-Dec-2005
? CLASSIFICATION: 530
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/978,773
? FILING DATE: 26-Nov-1997
? APPLICATION NUMBER: USSN 60/052,525
? FILING DATE: 27 NOVEMBER 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Perkins, Patricia Anne
? REGISTRATION NUMBER: 34,693
? REFERENCE/DOCKET NUMBER: 2623-A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206)587-0430
? TELEFAX: (206)
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 864 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 2:
? US-11-312-797-2

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Database : Published Applications AA Main:*

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- 2: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US10_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
93	386	100.0	73	US-10-063-742-30	Sequence 30, App1
168	386	100.0	73	US-10-013-909A-22	Sequence 22, App1
215	386	100.0	73	US-10-972-317-30	Sequence 30, App1
217	386	100.0	73	US-11-025-607-22	Sequence 22, App1
218	386	100.0	73	US-11-102-240-30	Sequence 30, App1
219	386	100.0	73	US-11-103-195-30	Sequence 30, App1
220	72	18.7	892	US-10-437-963-197731	Sequence 197731, App1
221	70.5	18.3	230	US-10-821-273-40	Sequence 40, App1
222	70.5	18.3	506	US-10-734-049A-270	Sequence 270, App1
223	69.5	18.0	225	US-10-243-552-601	Sequence 601, App1
224	68	17.6	930	US-09-918-171A-2	Sequence 2, App1
225	67.5	17.5	669	US-09-983-304-15	Sequence 15, App1
226	67.5	17.5	669	US-10-097-340-278	Sequence 280, App1
227	67.5	17.5	669	US-10-097-340-280	Sequence 280, App1
228	67.5	17.5	669	US-10-373-801-28	Sequence 28, App1
229	67.5	17.5	669	US-10-133-573-4	Sequence 4, App1
230	67.5	17.5	669	US-10-741-601-466	Sequence 466, App1
231	67.5	17.5	669	US-10-741-600-1350	Sequence 1350, App1
232	67.5	17.5	669	US-10-887-233-4	Sequence 4, App1
233	67.5	17.5	669	US-11-050-926-278	Sequence 278, App1
234	67.5	17.5	669	US-11-050-926-280	Sequence 280, App1
235	67	17.4	158	US-10-767-701-56878	Sequence 56878, App1
236	67	17.4	535	US-10-723-860-4109	Sequence 4109, App1
237	66.5	17.2	516	US-10-437-963-190239	Sequence 190239, App1
238	66.5	17.2	93	US-10-435-115-305253	Sequence 305253, App1
239	65.5	17.0	140	US-10-425-115-305253	Sequence 425, App1
240	65	16.8	475	US-10-243-552-629	Sequence 6, App1
241	65	16.8	475	US-10-312-315-6	Sequence 6, App1

242	65	16.8	475	US-10-509-464-8	Sequence 8, App1
243	64.5	16.7	172	US-10-437-963-143267	Sequence 143267, App1
244	64.5	16.7	245	US-10-450-763-52382	Sequence 52382, App1
245	64.5	16.7	526	US-10-437-963-143265	Sequence 143265, App1
246	64	16.6	379	US-10-369-493-3349	Sequence 3349, App1
247	63.5	16.5	81	US-10-311-129-34	Sequence 31, App1
248	63.5	16.5	96	US-10-425-115-301446	Sequence 301446, App1
249	63.5	16.5	125	US-10-986-405-299	Sequence 405, App1
250	63.5	16.5	137	US-10-986-405-302	Sequence 302, App1
251	63.5	16.5	158	US-10-425-115-311179	Sequence 311179, App1
252	63.5	16.5	225	US-10-002-631C-106	Sequence 106, App1
253	63.5	16.5	243	US-10-491-213-46	Sequence 46, App1
254	63.5	16.5	264	US-10-218-325-14	Sequence 50, App1
255	63.5	16.5	277	US-09-808-602-50	Sequence 40, App1
256	63.5	16.5	277	US-09-808-198-40	Sequence 66, App1
257	63.5	16.5	277	US-10-236-031B-66	Sequence 52, App1
258	63.5	16.5	282	US-09-808-602-52	Sequence 42, App1
259	63.5	16.5	282	US-09-800-198-42	Sequence 85, App1
260	63.5	16.5	282	US-10-301-822-85	Sequence 5, App1
261	63.5	16.5	282	US-10-418-064-5	Sequence 12, App1
262	63.5	16.5	282	US-10-240-240A-12	Sequence 19, App1
263	63.5	16.5	282	US-10-706-791-19	Sequence 101, App1
264	63.5	16.5	282	US-10-734-564-101	Sequence 14, App1
265	63.5	16.5	282	US-10-887-229A-14	Sequence 85, App1
266	63.5	16.5	282	US-11-186-284-85	Sequence 19413, App1
267	63.5	16.5	466	US-11-188-298-19413	Sequence 334402, App1
268	63	16.3	83	US-10-425-115-334402	Sequence 237205, App1
269	63	16.3	1896	US-10-312-352-34	Sequence 34, App1
270	63	16.3	1925	US-10-087-684-32	Sequence 32, App1
271	63	16.3	1925	US-10-218-779-39	Sequence 195983, App1
272	62	16.2	70	US-10-424-599-195983	Sequence 330866, App1
273	62.5	16.2	320	US-10-425-115-332086	Sequence 332086, App1
274	62.5	16.2	252	US-10-425-115-332836	Sequence 60040, App1
275	62	16.1	276	US-10-425-114-66040	Sequence 3003, App1
276	62	16.1	281	US-10-408-765A-3003	Sequence 10281, App1
277	62	16.1	349	US-11-098-686-10281	Sequence 10690, App1
278	62	16.1	356	US-10-156-761-10690	Sequence 1802, App1
279	62	16.1	837	US-10-389-566-1802	Sequence 17, App1
280	62	16.1	896	US-10-270-875-17	Sequence 17, App1
281	62	16.1	896	US-10-270-878-17	Sequence 17, App1
282	62	16.1	896	US-10-270-786-17	Sequence 17, App1
283	62	16.1	896	US-10-270-710-17	Sequence 17, App1
284	62	16.1	896	US-10-270-859-17	Sequence 17, App1
285	62	16.1	896	US-10-270-846-17	Sequence 2, App1
286	62	16.1	1238	US-09-904-065-2	Sequence 14, App1
287	62	16.1	1238	US-09-904-065-14	Sequence 2, App1
288	62	16.1	1238	US-10-692-556-12	Sequence 14, App1
289	62	16.1	1238	US-10-692-556-14	Sequence 14, App1
290	62	16.1	1238	US-10-692-556-14	Sequence 15, App1
291	62	16.1	1240	US-09-904-065-4	Sequence 4, App1
292	62	16.1	1240	US-09-904-065-15	Sequence 4, App1
293	62	16.1	1240	US-10-692-556-4	Sequence 4, App1
294	62	16.1	1240	US-10-692-556-15	Sequence 15, App1
295	61.5	15.9	144	US-10-424-599-284927	Sequence 284927, App1
296	61.5	15.9	167	US-10-425-115-218186	Sequence 218186, App1
297	61.5	15.9	184	US-10-264-237-1784	Sequence 1784, App1
298	61.5	15.9	279	US-10-424-599-240326	Sequence 240326, App1
299	61.5	15.9	402	US-10-450-763-32810	Sequence 32810, App1
300	61.5	15.9	630	US-11-188-298-19340	Sequence 19340, App1
301	61	15.8	152	US-09-800-729-84	Sequence 84, App1
302	61	15.8	152	US-09-833-245-2168	Sequence 2168, App1
303	61	15.8	152	US-11-264-096-2168	Sequence 2168, App1
304	61	15.8	185	US-10-425-115-331644	Sequence 331644, App1
305	61	15.8	327	US-10-437-963-194660	Sequence 194660, App1
306	60.5	15.7	125	US-10-767-701-51844	Sequence 51844, App1
307	60.5	15.7	136	US-10-094-749-2654	Sequence 2654, App1
308	60.5	15.7	147	US-10-425-115-240417	Sequence 240417, App1
309	60.5	15.7	280	US-10-073-300-6	Sequence 6, App1
310	60.5	15.7	280	US-10-075-257-6	Sequence 6, App1
311	60.5	15.7	365	US-10-138-888-23	Sequence 23, App1
312	60.5	15.7	365	US-10-741-601-325	Sequence 325, App1
313	60.5	15.7	365	US-10-741-601-326	Sequence 326, App1
314	60.5	15.7	365	US-10-741-600-939	Sequence 939, App1

315	60..5	15..7	365	5	US-10-741-600-940	Sequence 940, App	388	59	15..3	623	6	US-11-188-298-20491	Sequence 20491, A
316	60..5	15..7	365	5	US-10-821-324-1575	Sequence 1575, Ap	389	59	15..3	701	4	US-10-424-599-238593	Sequence 238593, App1
317	60.5	15.7	415	4	US-10-073-300-5	Sequence 5, App1	390	59	15.3	948	4	US-10-021-660-90	Sequence 93, App1
318	60.5	15.7	415	4	US-10-075-257-5	Sequence 5, App1	391	59	15.3	949	4	US-10-236-055A-22	Sequence 22, App1
319	60.5	15.7	421	6	US-11-040-686-42	Sequence 42, App1	392	59	15.3	949	4	US-10-211-662-30	Sequence 30, App1
320	60.5	15.7	510	4	US-10-108-511-5	Sequence 5, App1	393	59	15.3	967	4	US-10-425-114-54541	Sequence 54541, A
321	60.5	15.7	510	5	US-10-482-532-5	Sequence 5, App1	394	59	15.3	999	5	US-10-732-923-14198	Sequence 14199, A
322	60	15.5	94	4	US-10-437-963-170742	Sequence 5, App1	395	59	15.3	1043	5	US-10-424-599-281311	Sequence 281311, A
323	60	15.5	141	3	US-09-839-164-5	Sequence 5, App1	396	58.5	15.2	112	4	US-10-425-115-313028	Sequence 313028, A
324	60	15.5	141	4	US-10-128-581-24	Sequence 24, App1	397	58.5	15.2	114	4	US-10-097-065-245	Sequence 245, App
325	60	15.5	141	4	US-10-463-699-26	Sequence 26, App1	398	58.5	15.2	114	4	US-10-372-876-245	Sequence 251799, App
326	60	15.5	141	4	US-10-776-172-19	Sequence 19, App1	399	58.5	15.2	115	4	US-10-425-115-251799	Sequence 193424, App
327	60	15.5	141	5	US-10-897-005-26	Sequence 26, App1	400	58.5	15.2	124	4	US-10-425-115-193424	Sequence 203944, App
328	60	15.5	142	5	US-10-979-483-22	Sequence 22, App1	401	58.5	15.2	202	4	US-10-425-115-203944	Sequence 55, App1
329	60	15.5	169	4	US-10-425-114-62126	Sequence 62126, A	402	58.5	15.2	216	4	US-10-332-947-55	Sequence 2, App1
330	60	15.5	169	4	US-10-425-114-62127	Sequence 62127, A	403	58.5	15.2	331	3	US-09-033-525-2	Sequence 2, App1
331	60	15.5	461	5	US-10-509-464-7	Sequence 7, App1	404	58.5	15.2	331	5	US-10-640-668-2	Sequence 2, App1
332	60	15.5	826	5	US-10-778-804-10	Sequence 10, App1	405	58.5	15.2	335	5	US-10-287-436A-179	Sequence 179, App
333	59.5	15.4	58	3	US-09-974-879-261	Sequence 261, App	406	58.5	15.2	355	5	US-10-287-436A-1268	Sequence 1268, App
334	59.5	15.4	58	4	US-10-621-401-261	Sequence 261, App	407	58.5	15.2	459	4	US-10-156-761-11304	Sequence 11304, A
335	59.5	15.4	59	3	US-09-305-736-261	Sequence 261, App	408	58	15.0	111	4	US-10-424-599-279650	Sequence 279650, App
336	59.5	15.4	59	3	US-09-818-683-261	Sequence 261, App	409	58	15.0	123	3	US-09-693-737-90	Sequence 90, App1
337	59.5	15.4	59	3	US-09-818-683-261	Sequence 261, App	410	58	15.0	123	5	US-10-970-713-90	Sequence 90, App1
338	59.5	15.4	167	4	US-10-437-963-106334	Sequence 106334, A	411	58	15.0	188	4	US-10-437-963-157602	Sequence 157602, App
339	59.5	15.4	202	4	US-10-437-963-112018	Sequence 112018, A	412	58	15.0	151	4	US-10-767-701-35067	Sequence 35067, A
340	59.5	15.4	291	4	US-10-437-963-171523	Sequence 171523, A	413	58	15.0	201	3	US-09-764-875-715	Sequence 715, App
341	59.5	15.4	430	4	US-10-156-761-14016	Sequence 14016, A	414	58	15.0	285	4	US-10-458-143-16	Sequence 16, App1
342	59.5	15.4	444	4	US-10-087-192-1512	Sequence 1512, Ap	415	58	15.0	309	3	US-09-892-074-2	Sequence 64936, A
343	59.5	15.4	446	5	US-10-852-335A-169	Sequence 169, App	416	58	15.0	329	3	US-10-425-114-64936	Sequence 2, App1
344	59.5	15.4	446	5	US-10-287-436A-433	Sequence 433, App	417	58	15.0	379	4	US-10-118-661-6	Sequence 65606, A
345	59.5	15.4	446	5	US-10-287-436A-1134	Sequence 1134, Ap	418	58	15.0	444	4	US-10-318-661-6	Sequence 6, App1
346	59.5	15.4	481	5	US-10-437-963-195459	Sequence 195459, A	419	58	15.0	444	4	US-10-318-661-6	Sequence 8, App1
347	59.5	15.4	613	4	US-10-437-963-106249	Sequence 106249, A	420	58	15.0	427	4	US-10-118-661-4	Sequence 4, App1
348	59.5	15.4	741	4	US-10-437-963-193189	Sequence 193189, A	421	58	15.0	437	4	US-10-167-749-90	Sequence 90, App1
349	59.5	15.4	793	4	US-10-408-765A-2754	Sequence 2754, Ap	422	58	15.0	432	4	US-10-174-587-74	Sequence 74, App1
350	59.5	15.4	2462	3	US-09-819-104A-5	Sequence 5, App1	423	58	15.0	432	4	US-10-174-587-74	Sequence 90, App1
351	59	15.3	99	4	US-10-425-115-297128	Sequence 297128, A	424	58	15.0	432	4	US-10-210-028-90	Sequence 90, App1
352	59	15.3	102	4	US-10-437-963-139626	Sequence 139626, A	425	58	15.0	432	4	US-10-162-521A-90	Sequence 90, App1
353	59	15.3	107	4	US-10-115-482-54	Sequence 54, App1	426	58	15.0	432	5	US-10-918-851-90	Sequence 90, App1
354	59	15.3	122	4	US-10-115-482-52	Sequence 52, App1	427	58	15.0	432	5	US-10-805-667-90	Sequence 90, App1
355	59	15.3	141	3	US-09-839-154-2	Sequence 2, App1	428	58	15.0	432	5	US-10-805-667-90	Sequence 90, App1
356	59	15.3	141	3	US-09-977-577-14	Sequence 14, App1	429	58	15.0	432	5	US-10-897-359-90	Sequence 90, App1
357	59	15.3	141	4	US-10-085-853-21	Sequence 21, App1	430	58	15.0	432	5	US-10-897-360-90	Sequence 90, App1
358	59	15.3	141	4	US-10-128-581-21	Sequence 21, App1	431	58	15.0	432	5	US-10-935-752-2	Sequence 2, App1
359	59	15.3	141	4	US-10-128-581-21	Sequence 21, App1	432	58	15.0	432	5	US-10-935-752-2	Sequence 3, App1
360	59	15.3	141	4	US-10-280-679B-8	Sequence 8, App1	433	58	15.0	432	5	US-10-501-841-45	Sequence 45, App1
361	59	15.3	141	4	US-10-280-679B-8	Sequence 8, App1	434	58	15.0	432	6	US-11-129-762-90	Sequence 90, App1
362	59	15.3	141	4	US-10-463-689-23	Sequence 23, App1	435	58	15.0	432	6	US-10-450-763-59260	Sequence 59260, A
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364	59	15.3	141	5	US-10-776-172-16	Sequence 16, App1	437	58	15.0	642	3	US-09-815-242-11810	Sequence 696, App
365	59	15.3	141	5	US-10-897-005-23	Sequence 23, App1	438	58	15.0	1873	5	US-10-784-004-696	Sequence 710, App
366	59	15.3	141	5	US-10-885-784-14	Sequence 14, App1	439	58	15.0	1873	5	US-10-784-004-696	Sequence 710, App
367	59	15.3	142	4	US-10-435-666-7	Sequence 7, App1	440	57.5	14.9	69	4	US-10-425-115-195415	Sequence 195415, A
368	59	15.3	142	4	US-10-425-115-49126	Sequence 249126, A	441	57.5	14.9	73	4	US-10-424-599-145604	Sequence 145604, A
369	59	15.3	142	5	US-10-287-436A-446	Sequence 446, App	442	57.5	14.9	74	4	US-10-013-809A-189	Sequence 189, App
370	59	15.3	142	5	US-10-287-436A-1254	Sequence 1254, Ap	443	57.5	14.9	74	6	US-11-025-607-189	Sequence 189, App
371	59	15.3	145	5	US-10-994-612-79	Sequence 79, App1	444	57.5	14.9	102	4	US-10-425-115-264739	Sequence 264739, App
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373	59	15.3	160	5	US-10-821-234-863	Sequence 863, App	446	57.5	14.9	110	4	US-10-767-701-42617	Sequence 42617, A
374	59	15.3	190	5	US-10-972-024-151	Sequence 151, App	447	57.5	14.9	215	3	US-10-437-963-203545	Sequence 203545, App
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380	59	15.3	333	4	US-10-206-401-2	Sequence 2, App1	453	57.5	14.9	385	4	US-10-000-512-14	Sequence 14, App1
381	59	15.3	333	4	US-10-239-423-83	Sequence 83, App1	454	57.5	14.9	385	4	US-10-074-566-14	Sequence 14, App1
382	59	15.3	333	5	US-10-925-095-509	Sequence 509, App	455	57.5	14.9	385	4	US-10-074-566-49	Sequence 49, App1
383	59	15.3	333	6	US-11-127-877-57	Sequence 57, App1	456	57.5	14.9	385	4	US-10-074-566-78	Sequence 78, App1
384	59	15.3	339	5	US-10-220-335-250	Sequence 250, App	457	57.5	14.9	385	5	US-10-658-213-16	Sequence 16, App1
385	59	15.3	465	4	US-10-094-749-1663	Sequence 1663, Ap	458	57.5	14.9	385	5	US-10-973-858-26	Sequence 26, App1
386	59	15.3	480	6	US-11-096-568A-13350	Sequence 13350, A	459	57.5	14.9	468	4	US-10-453-195-14	Sequence 14, App1
387	59	15.3	488	4	US-10-097-065-140	Sequence 140, App	460	57.5	14.9	468	4	US-10-453-195-14	Sequence 14, App1
			488	4	US-10-372-876-140	Sequence 140, App	461	57.5	14.9	471	3	US-09-893-737-186	Sequence 186, App

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1140	57.5	14.9	561	4	US-10-425-115-316538	Sequence 316538,
1141	57.5	14.9	652	3	US-09-992-647-1	Sequence 1, Appli
1142	57.5	14.9	652	4	US-10-225-567A-653	Sequence 653, App
1143	57.5	14.9	652	4	US-10-436-715-65	Sequence 65, Appl
1144	57.5	14.9	655	4	US-10-437-963-135522	Sequence 135522,
1145	57.5	14.9	661	3	US-09-764-893-114	Sequence 114, App
1146	57.5	14.9	661	3	US-09-764-853-679	Sequence 679, App
1147	57.5	14.9	661	3	US-09-764-898-224	Sequence 224, App
1148	57.5	14.9	661	4	US-10-073-865-114	Sequence 114, App
1149	57.5	14.9	890	5	US-10-505-486-33	Sequence 33, Appl
1150	57.5	14.9	960	6	US-11-097-143-3159	Sequence 3159, App
1151	57.5	14.9	960	6	US-11-097-143-26145	Sequence 26145, A
1152	57.5	14.9	960	6	US-11-097-143-26148	Sequence 26148, A
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)
125.289 Million cell updates/sec

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Perfect score: 386
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Scoring table: BLOSUM62

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	386	100.0	73	2	US-10-015-389A-22
3	386	100.0	73	2	US-10-006-768A-22
4	386	100.0	73	2	US-10-015-671A-22
5	386	100.0	73	2	US-10-015-393A-22
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7	386	100.0	73	2	US-10-006-041A-22
8	386	100.0	73	2	US-10-012-064A-22
9	386	100.0	73	2	US-10-015-392A-22
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11	386	100.0	73	3	US-10-015-386A-22
12	386	100.0	73	3	US-10-012-121A-22
13	386	100.0	73	3	US-10-006-485A-22
14	386	100.0	73	3	US-10-006-746A-22
15	386	100.0	73	3	US-10-012-752A-22
16	386	100.0	73	3	US-10-017-253A-22
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19	386	100.0	73	3	US-10-007-236A-22
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22	72	18.7	884	1	US-08-983-412-2
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25	63.5	16.5	282	2	US-09-461-912A-38
26	62.5	16.2	270	1	US-08-978-404B-8

27	62.5	16.2	307	2	US-09-252-991A-32304	Sequence 32304, A
28	62	16.1	484	2	US-09-248-796A-17959	Sequence 17959, A
29	62	16.1	896	2	US-09-585-858-17	Sequence 17, Appl
30	62	16.1	896	2	US-10-270-878-17	Sequence 17, Appl
31	62	16.1	1238	2	US-09-904-065-2	Sequence 2, Appl
32	62	16.1	1238	2	US-09-904-065-14	Sequence 14, Appl
33	62	16.1	1240	2	US-08-680-326-37	Sequence 37, Appl
34	62	16.1	1240	2	US-09-904-065-4	Sequence 4, Appl
35	62	16.1	1240	2	US-09-904-065-15	Sequence 15, Appl
36	61.5	15.9	578	2	US-09-503-172A-2	Sequence 2, Appl
37	61	15.8	152	2	US-08-800-729-84	Sequence 84, Appl
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40	60.5	15.7	274	1	US-08-484-905-107	Sequence 107, App
41	60.5	15.7	274	1	US-08-484-905-108	Sequence 108, App
42	60.5	15.7	274	2	US-08-481-985B-107	Sequence 105, App
43	60.5	15.7	274	2	US-08-481-985B-107	Sequence 107, App
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45	60.5	15.7	274	2	US-08-370-476-105	Sequence 105, App

ALIGNMENTS

RESULT 1
US-10-012-231A-22
Sequence 22, Application US/10012231A
Patent No. 6924355
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Boetstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PIC23
CURRENT APPLICATION NUMBER: US/10/012,231A
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
NAME/KEY: misc feature
LOCATION: 3-18
OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-231A-22
Query Match 100.0%; Score 386; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLLTLLTLKSGSCLWVGAOKVSSATAPIDMFPFSPICLPHRAMCSQ 60
OY 61 AQRGEKVGQDG 73

Db 61 AOPRGESEKVG DG 73

RESULT 2

US-10-015-389A-22
Sequence 22, Application US/10015389A
Patent No. 6936436
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C48
CURRENT APPLICATION NUMBER: US/10/015,389A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3-18
OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-389A-22

Query Match 100.0%; Score 386; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1,4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MLTLTLLTLKSGCLEWGLVGAQKVSATDAPIRDMAFPPSPFLCLLPHRPAMTCSQ 60
QY 61 AOPRGESEKVG DG 73
Db 61 AOPRGESEKVG DG 73

RESULT 3

US-10-006-768A-22
Sequence 22, Application US/10006768A
Patent No. 6936697
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C10
CURRENT APPLICATION NUMBER: US/10/006,768A
CURRENT FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 477
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3-18
OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-006-768A-22

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Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AOPRGESEKVG DG 73
Db 61 AOPRGESEKVG DG 73

RESULT 4

US-10-015-671A-22
Sequence 22, Application US/10015671A
Patent No. 6946263
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C47
CURRENT APPLICATION NUMBER: US/10/015,671A
CURRENT FILING DATE: 2001-12-11
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 22
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1-15
OTHER INFORMATION: Signal peptide.
FEATURE:
NAME/KEY: misc_feature

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; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-671A-22

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Best Local Similarity 100.0%; Pred. No. 1.4e-43;
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QY 61 AQRGEGEKVGDG 73
DB 61 AQRGEGEKVGDG 73

RESULT 5
US-10-015-393A-22
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; Patent No. 6951737
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; PRIOR FILING DATE: 2002-06-10
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; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-393A-22

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US-10-011-833A-22
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C22
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; PRIOR FILING DATE: 2002-06-25
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; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
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; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-011-833A-22

Query Match      100.0%; Score 386; DB 2; Length 73;
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QY 61 AQRGEGEKVGDG 73
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RESULT 7
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; Patent No. 6951921
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A
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; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
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; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
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; NAME/KEY: sig_peptide
; LOCATION: 1-15
; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-006-041A-22
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Query Match 100.0%; Score 386; DB 2; Length 73;
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; Patent No. 6953841
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C19
; CURRENT APPLICATION NUMBER: US/10/012,064A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
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; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
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; PRIOR APPLICATION NUMBER: 60/099536
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; PRIOR FILING DATE: 1998-09-09
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; FEATURE:
; NAME/KEY: sig_peptide
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; OTHER INFORMATION: Signal peptide.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3-18
; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-012-064A-22
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Query Match 100.0%; Score 386; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1,4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 AQPREGGEKVG DG 73
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US-10-015-392A-22
; Sequence 22, Application US/10015392A
; Patent No. 6972186
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C58
; CURRENT APPLICATION NUMBER: US/10/015,392A
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
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; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
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;; PRIOR FILING DATE: 1998-09-09
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 22
;; LENGTH: 73
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig peptide
;; LOCATION: 1-15
;; OTHER INFORMATION: Signal peptide.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 3-18
;; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-015-392A-22

Query Match 100.0%; Score 386; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10

US-10-011-795B-22
;; Sequence 22, Application US/10011795B
;; Patent No. 7012131

;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eaton, Dan I.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2830P1C5
;; CURRENT APPLICATION NUMBER: US/10/011.795B
;; PRIOR FILING DATE: 2001-12-07
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;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099598

;; PRIOR FILING DATE: 1998-09-09
;; Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 477
;; SEQ ID NO 22
;; LENGTH: 73
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig peptide
;; LOCATION: 1-15
;; OTHER INFORMATION: Signal peptide.
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 3-18
;; OTHER INFORMATION: Growth factor and cytokines receptors family.
US-10-011-795B-22

Query Match 100.0%; Score 386; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.4e-43;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AOPRGEGERVGDG 73
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RESULT 11

US-10-015-386A-22
;; Sequence 22, Application US/10015386A
;; Patent No. 7022498

;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eaton, Dan I.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, Christopher J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2830P1C5
;; CURRENT APPLICATION NUMBER: US/10/015.386A
;; PRIOR FILING DATE: 2001-12-12
;; PRIOR APPLICATION NUMBER: 60/098716
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;; PRIOR FILING DATE: 1998-10-28

Query Match 100.0%; Score 386; DB 3; Length 73;
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Db 1 MLTLTLLLLLLKSGCLEMGLVGAQKVSSATDAPFIDMAFFPPSFCLLPHRPAMTCGQ 60

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RESULT 14
US-10-006-746A-22 Application US/10006746A
Patent No. 7026449
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan I.
APPLICANT: Ferrata, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P15
CURRENT APPLICATION NUMBER: US/10/006,746A
CURRENT FILING DATE: 2001-12-06
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Query Match          100.0%; Score 386; DB 3; Length 73;
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Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 15
US-10-012-752A-22
/ Sequence 22, Application US/10012752A
/ Patent No. 7026455
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Bocstein, David
/ APPLICANT: Deenoyers, Luc
/ APPLICANT: Eaton, Dan I.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
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/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2830P1C24
/ CURRENT APPLICATION NUMBER: US/10/012,752A
/ CURRENT FILING DATE: 2002-06-25
/ Prior application removed - See file Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 477
/ SEQ ID NO 22
/ LENGTH: 73
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 1-15
/ OTHER INFORMATION: Signal peptide.
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/ NAME/KEY: misc_feature
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/ OTHER INFORMATION: Growth factor and cytokines receptors family.
/ US-10-012-752A-22
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Query Match          100.0%; Score 386; DB 3; Length 73;
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Job time : 52 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: June 6, 2006, 21:30:19 ; Search time 294 Seconds

(without alignments)
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Title: US-10-063-534-30

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Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result (No.)	Score	Query Match Length	ID	Description
1	386	100.0	73	06UWT3 HUMAN
2	85	22.0	144	04S4U9 TETNG
3	77	19.9	116	08T3M4 DROME
4	77	19.9	125	08IR67 DROME
5	75.5	19.6	468	04V7Z1 XENLA
6	73.5	19.0	379	06D1J0 XENTR
7	72	18.7	892	053P51 ORYSA
8	71.5	18.5	1912	09ERCI RAT
9	71	18.4	878	04D8X5 TRYCR
10	70.5	18.3	506	04S4U9 TETNG
11	70.5	18.3	506	04S4U9 TETNG
12	70	18.1	257	05K5P3 PONPY
13	69.5	18.0	130	06IGC8 DROME
14	69	17.9	462	1 KREMG HUMAN
15	69	17.9	652	04RTS7 TETNG
16	68	17.6	307	07S7R5 NEUCR
17	68	17.6	725	08CB87 MOUSE
18	68	17.6	930	08CB87 MOUSE
19	67.5	17.5	669	06G5G6 HUMAN
20	67.5	17.5	669	06G5G6 HUMAN
21	67.5	17.5	3898	02UAI4 ASPOR
22	67.5	17.5	5255	02PC93 CHICK
23	67	17.4	159	07PL12 ANOGA
24	67	17.4	159	07PL12 ANOGA
25	67	17.4	351	07ZAN6 DESVI
26	67	17.4	535	0215175 HUMAN
27	66.5	17.2	557	06G5M3 BARHE
28	66	17.1	771	09RIE7 MOUSE
29	66	17.1	368	089R59 BRAJA
30	66	17.1	385	031IK8 THICR
31	66	17.1	482	05ZBR9 ORYSA

32	65.5	17.0	92	03K6Z7 PSEPR	03K6Z7 pseudomonas
33	65.5	17.0	223	0315Y9 DESDG	0315Y9 desulfovibr
34	65.5	17.0	3788	09Z2X9 RAT	09Z2X9 rattus norv
35	65	16.8	157	08T6R9 ANOGA	08T6R9 anopheles g
36	65	16.8	1327	02P0Z1 XANOR	02P0Z1 xanthomonas
37	64.5	16.7	207	05UN21 ORYSA	05UN21 oryza sativ
38	64.5	16.7	407	07W14 BORPE	07W14 bordetella
39	64.5	16.7	407	07W553 BORPA	07W553 bordetella
40	64.5	16.7	407	07WCNS BORBR	07WCNS bordetella
41	64	16.6	103	07U7R9 SYNXP	07U7R9 synecococc
42	64	16.6	164	05T5A0 HUMAN	05T5A0 homo sapien
43	64	16.6	210	06I177 DROME	06I177 drosophila
44	64	16.6	862	04PCZ1 USTMA	04PCZ1 utililago ma
45	64	16.6	1029	07S2D9 NEUCR	07S2D9 neurospora

ALIGNMENTS

RESULT 1	06UWT3 HUMAN	PRELIMINARY;	PRT;	73 AA.
AC	06UWT3			
DT	05-JUL-2004, integrated into UniProtKB/TrEMBL.			
DT	05-JUL-2004, sequence version 1.			
DT	07-FEB-2006, entry version 7.			
DE	APPLIN			
GN	ORRNames=UNQ471;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,			
RA	Chen Y., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,			
RA	Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,			
RA	Seehaghi S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vanclen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,			
RA	Yasusara D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,			
RA	Wood W.I., Godowski P.J., Gray A.M.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonDerivs license			
CC	EMBL; AY358657; AA089020.1; -; mRNA.			
DR	SEQUENCE 73 AA; 7879 MW; A99C6797BCAD91 CRC64;			
SO	SEQUENCE			
Query Match	100.0%;	Score 386;	DB 2;	Length 73;
Best local Similarity	100.0%;	Pred. No. 3.7e-37;		
Matches	73;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps	0;			
OR	1 MLTLTLLTLLLLKSGCLEWGAQKYSSATDAPIRDMAFPPSPFCLLPHRPAATCSQ 60			
DB	1 MLTLTLLTLLLLKSGCLEWGAQKYSSATDAPIRDMAFPPSPFCLLPHRPAATCSQ 60			
OR	61 AOPRGESEKVGDG 73			
DB	61 AOPRGESEKVGDG 73			
RESULT 2	04S4U9 TETNG	PRELIMINARY;	PRT;	144 AA.
ID	04S4U9			
AC	04S4U9			

DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 19-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Chromosome 2 SCRF14738, whole genome shotgun sequence. (Fragment).
 GN ORFNames=GSTENG0024149001;
 OS Tetradon nigriviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 NC NCB1_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15496914; DOI=10.1038/nature03025;
 RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,
 RA Mucelli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicolas S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dastiva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Cactolico L., Poullain J., De Bernardis V.,
 RA Cruaud C., Duprat S., Broctier P., Coutanceau J.-P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Westrov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissenbach J., Roest Crollius H.,
 RA "Genome duplication in the teleost fish Tetraodon nigriviridis reveals
 RT the early vertebrate proto-karyotype".
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 DR EMBL, CAAB01014738, CAG04433.1; -, Genomic DNA.
 FT NON_TER 144 144
 SQ SEQUENCE 144 AA; 15706 MW; 420C361E7905419D CRC64;
 QY Query Match 22.0%; Score 85; DB 2; Length 144;
 Best Local Similarity 38.6%; Pred. No. 0.12;
 Matches 21; Conservative 8; Mismatches 29; Indels 6; Gaps 2;
 QY 1 MLLLTLLLLLLKSGSCLWGLVGAQKVSATDAPIRDMAFFPPSPFLCLPHRPAMTCSQ 60
 Db 6 VLLPLSTLVLLLGTC---GLVSLAQSRLTLATASFFPICKTFCCLPKKCSFTLS- 61
 QY 61 AQRGEGEKV 70
 Db 62 --PRTEGVAV 69
 DE CM087889 (Fragment).
 GN ORFNames=CG32634;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
 RA Ceinlier S.,
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL, AY094760, AAM1113.1; -, mRNA.
 DR FLYBase; FBgn0052634; CG32634.
 FT NON_TER 1
 SQ SEQUENCE 116 AA; 12750 MW; 94A6D36789A712BD CRC64;
 QY Query Match 19.9%; Score 77; DB 2; Length 116;
 Best Local Similarity 37.3%; Pred. No. 0.83;
 Matches 19; Conservative 9; Mismatches 19; Indels 4; Gaps 1;
 QY 1 MLLLTLLLLLLKSGSCLWGLVGAQKVSATDAPIRDMAFFPPSPFLCLP 51
 Db 64 LLLLLLLLLLLQ-----QHLAASQIDLEAKPLVDFLVPLSSCTFP 110
 RESULT 4
 QY 081R67_DROME PRELIMINARY; PRT; 125 AA.
 AC 081R67_2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE CG32634-PA.
 GN ORFNames=CG32634; Dmel.CG32634;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10711132; DOI=10.1126/science.287.5461.2185;
 RA Adams W.D., Ceinlier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Morten J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mayhew A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
 RA Jajuel M.E., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puig V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Javerly T., Muzny D.M., Nelson C.R.,
RA Pavlel J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svrtkas R., Taber P.E., Man K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svrtkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Ceiniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktiroglu L., Bertman B.P.,
RA Bellocourt B.R., Ceiniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
[5]
RN NUCLEOTIDE SEQUENCE.
RP Berkeley Drosophila Genome Project;
RA Ceiniker S., Carlson J., Man K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pavlel J., Park S., Svrtkas R., Smith B.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP FlyBase;
RL Submitted (JUN-2006) to the EMBL/GenBank/DBJ databases.
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CC EMBL, AE003492; AAND09329.1; -; Genomic_DNA.
DR FlyBase; FBgn0052634; CG32634.
SQ SEQUENCE 125 AA; 13934 MW; 33654FFB0C2852C9 CRC64;
Query Match 19.9%; Score 77; DB 2; Length 125;
Best Local Similarity 37.3%; Pred. No. 0.89; Mismatches 19; Indels 4; Gaps 1;
Matches 19; Conservative 9; Mismatches 19; Indels 4; Gaps 1;
Qy 1 MLTLLTLLTLLKSCLEWGLVGAQKVSATDAPIRDAFPFPPSFLCLLP 51
Db 73 LTLTLLTLLTLLTQ-----QETLAAQQQLDEAKRPLVDFLLVPLPSSCTFP 119
RESULT 5
Q4V721_XENLA PRELIMINARY; PRT; 468 AA.
ID Q4V721_XENLA

Q4V721;
AC 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8335;
RN (1)
RN NUCLEOTIDE SEQUENCE.
RP TISSUE-Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*
Initiative.";
RL Dev. Dyn. 225:384-391(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE-Ovary;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Umed T.B., Toshimiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman W., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE-Ovary;
RC Klein S., Gerhard D.S.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
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CC EMBL, BC097649; AA97649.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR PROSITE; PS00320; WD40; 7.
DR SMART; SMO0320; WD40; 7.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 468 AA; 52116 MW; 35C18B58D2E5564 CRC64;
Query Match 19.6%; Score 75.5; DB 2; Length 468;
Best Local Similarity 35.3%; Pred. No. 4.8;
Matches 18; Conservative 8; Mismatches 24; Indels 1; Gaps 1;
Qy 16 SCLEWGLVGAQKVSATDAPIRDAFPFPPSFLCLLP--HRPAMTCQAQAPRG 65
Db 22 TCVDFSPDSKQLASSADACVMTWFKQSRAYKYPGAKAVTCVQPSFG 72

```

RESULT 6
06DJUO_XENTR PRELIMINARY; PRT: 379 AA.
ID O6DJUO_XENTR PRELIMINARY; PRT: 379 AA.
AC O6DJUO;
DT 16-AUG-2004, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE MGC89488 protein.
GN Name=MGC89488;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Silurana.
OX NCBI_Taxid=8364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzetta K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.A., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skolka U., Smallus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99.16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC075348; AA075348.1; -; mRNA.
DR Ensembl; ENSXETG0000021865; Xenopus tropicalis.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 7.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 379 AA; 42159 MW; 985760337D2D8523 CRC64;

Query Match 19.0%; Score 73.5; DB 2; Length 379;
Best Local Similarity 41.9%; Pred. No. 6.7;
Matches 18; Conservative 4; Mismatches 20; Indels 1; Gaps 1;

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DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Hypothetical protein.
GN ORFNames=LOC_0811908400;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,
RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Taitlin T.,
RA Bera J., Kim M., Jin S., Padrosh D., Vuong H., Overton II L.,
RA Reardon M., Weaver B., Johri S., Lewis M., Urtchack T., Van Aken S.,
RA Wortman J., Haas B., Koo H., Ziemann V., Hsiao J., Iobst S.,
RA de Vazellees A., White O., Salzberg S., Fraser C.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Buell R.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AC128644; AA96348.1; -; Genomic DNA.
DR EMBL; DP000010; AB91822.1; -; Genomic DNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00320; GPROTEINRPT.
DR PRODOM; PD000018; WD40; 3.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 892 AA; 96390 MW; D60827E1D11C11 CRC64;

Query Match 18.7%; Score 72; DB 2; Length 892;
Best Local Similarity 32.0%; Pred. No. 23;
Matches 16; Conservative 7; Mismatches 27; Indels 0; Gaps 0;

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RESULT 7
053P51_ORYSA PRELIMINARY; PRT: 892 AA.
ID 053P51_ORYSA PRELIMINARY; PRT: 892 AA.
AC 053P51;

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QY 24 GAQKVSATDPAIRDMAFPSPFLCLP-HRPAMTCSQAQPRG 65
DB 30 GKQLASSADACVMIWNFKPQSAVKYKYGKAEAVTCVQFSPSG 72

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RESULT 8
Q9ERC1_RAT PRELIMINARY; PRT: 1912 AA.
ID Q9ERC1_RAT PRELIMINARY; PRT: 1912 AA.
AC Q9ERC1;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE Myosin heavy chain Myr 8b.
GN Name=Loc192253;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21472394; PubMed=11588169;
RA Patel K.G., Liu C., Cameron F.L., Cameron R.S.;
RT "Myr 8, a novel unconventional myosin expressed during brain

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RT development associates with the protein phosphatase catalytic subunits
 RT lalpha and lgamma1.";
 RL J. Neurosci. 21:7954-7968(2001).
 CC -----
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 CC -----
 CC EMBL: AY004215; AAC23288.1; -; mRNA.
 DR HSSP: P08799; 1MND.
 DR Ensemble: ENSRNOG0000016483; Rattus norvegicus.
 DR RGD: 621561; LOC192253.
 DR GO: GO:0016459; C:myosin; IDA.
 DR GO: GO:0003779; F:actin binding; IDA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000048; IQ Cam bd region.
 DR InterPro: IPR01609; Myosin_head.
 DR Pfam: PF00023; Ank; 6.
 DR Pfam: PF00612; IQ; 1.
 DR Pfam: PF00063; Myosin_head; 2.
 DR PRINTS: PR01415; ANKYRIN.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; Myosin_head; 1.
 DR SMART: SM00248; ANK; 4.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50088; ANK_REPEAT; 4.
 DR PROSITE: PS50096; IQ; 1.
 SQ SEQUENCE 1912 AA; 210691 MW; 7C15014A1A83C9C3 CRC64;
 Query Match 18.5%; Score 71.5; DB 2; Length 1912;
 Best Local Similarity 34.7%; Pred. No. 55;
 Matches 25; Conservative 4; Mismatches 22; Indels 21; Gaps 3;
 QY 3 LTLTL-----LTLTLKSGSLEWLVGAQVSSATDPIFDMAFPPSPFLCLPHRAM- 56
 DB 1457 MTLFPLASPLFLFETRAAILLEAGEGSCQ-----PLKDTCDIPPPFLLPHRPLL 1508
 QY 57 -----TCSQA 61
 DB 1509 VFPPPTVTCSPA 1520
 Db
 RESULT 9
 Q4DBX5_TRYCR PRELIMINARY; PRT; 878 AA.
 AC Q4DBX5;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE Hypothetical protein.
 GN ORFNames=TC00.1047053506587.20;
 OS Trypanosoma cruzi.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
 OC Schizotrypanum.
 NCBI TaxId=5693;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CL Brenner;
 RA El-Sayed N.M.A., Myler P.J., Bartholomew D.C., Nilsson D.,
 RA Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,
 RA Blandin G., Westembarger S.J., Caler E., Cerqueira G.C., Branche C.,
 RA Haas B., Anandana A., Arner E., Aslund L., Altjoe P., Bontempo E.,
 RA Brindaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,
 RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,
 RA Englund P.T., Fazellina G., Feldblum T., Ferrelia M., Frasch A.C.,
 RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,
 RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,
 RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,
 RA Nelson S., Ochaya S., Osogawa K., Pai G., Parsons M., Pencony M.,
 RA Petersen U., Pop M., Ramirez J.L., Rinta J., Robertson L.,
 RA Salzman S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,
 RA Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
 RA Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O.,

RA Fraser C.M., Stuart K.D., Andersson B.;
 RT "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas'
 RT Disease";
 RL Science 0:0-0(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CL Brenner;
 RA El-Sayed N.M.A., Myler P.J., Blandin G., Berrihan M., Crabtree J.,
 RA Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
 RA Ghedin E., Peacock C., Bartholomew D.C., Haas B.J., Tran A.-N.,
 RA Wortman J.R., Alsmark U.C.M., Angiuoli S., Anandana A., Badger J.,
 RA Brindaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
 RA Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
 RA Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
 RA Salzberg S.L., Shallow J., Silva J.C., Sundaram S., Westembarger S.,
 RA White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
 RA Hall N.;
 RT "Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
 RL Science 0:0-0(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CL Brenner;
 RA El-Sayed N., Bartholomew D., Haas B.;
 RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RL -i- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
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 CC -----
 CC EMBL: AAHK01000802; EAM88969.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 878 AA; 97344 MW; 6CA2E07991B4379 CRC64;
 Query Match 18.4%; Score 71; DB 2; Length 878;
 Best Local Similarity 27.4%; Pred. No. 30;
 Matches 20; Conservative 9; Mismatches 22; Indels 22; Gaps 2;
 QY 5 TLLTLTLKSGSLEWLVGAQVSSATDPIFDMAFPPSPFLCL- 52
 DB 796 TLVTLVLLNSGTC-----VGLSDGKVDLGLSPSSLSPLSGTGLTIEDLPH 845
 QY 53 RPAMTCSQAQPRG 65
 DB 846 VSSLTMRHAYKNG 858
 Db
 RESULT 10
 CKSP3_HUMAN STANDARD; PRT; 506 AA.
 AC Q96JB5; Q53FA2; Q9H3F8; Q9H8G0; Q9HBR9; Q9HBR9; Swiss-Prot.
 DT 16-JUN-2003, integrated into UniProtKB/Swiss-Prot.
 DT 16-JUN-2003, sequence version 2.
 DT 07-MAR-2006, entry version 30.
 DE CDK5 regulatory subunit-associated protein 3 (CDK5 activator-binding
 DE protein C53) (HSP-27 protein).
 GN Name=CDK5RAP3; Synonyms=IC53; ORFNames=MSTRP016, OK/SW-cl.114, PPI553;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 2), AND TISSUE SPECIFICITY.
 RC TISSUE=Aorta;
 RX MEDLINE=22050200; Pubmed=12054757; DOI=10.1016/S0006-291X(02)00446-1;
 RA Chen J., Liu B., Liu Y.Q., Han Y., Yu H., Zhang Y., Lu L., Zhen Y.,
 RA Hui R.T.;
 RT "A novel gene IC53 stimulates ECV304 cell proliferation and is
 RT upregulated in failing heart.";
 RL Biochem. Biophys. Res. Commun. 294:161-166(2002).
 RN [2]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 3), FUNCTION, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=Placenta;
 RX PubMed=12737517;
 RA Xie Y.H., He X.H., Tang Y.T., Li J.J., Pan Z.M., Qin W.X., Wan da F.,
 RA Gu J.R.;
 RT "Cloning and characterization of human IC53-2, a novel CDK5 activator
 RT binding protein.";
 RL Cell Res. 13:83-91(2003).
 RN
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RC TISSUE=Kidney;
 RA Favier A.-L., Harzi C., Chroboczek J.;
 RT "Protein interacting with the receptor binding domain of enteric
 RT adenovirus serotype 41 fiber protein.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Colon adenocarcinoma;
 RA Shichijo S., Itoh K.;
 RT "Identification of immuno-peptidomimics that are recognized by tumor-
 RT reactive CTL generated from TIL of colon cancer patients.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano Y.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita H., Imose N.,
 RA Moshahiro K., Yuuki H., Oshima H., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto K., Kawakami B.,
 RA Yamagaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujimura T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hara H., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Mizushima K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Synovial cell;
 RA Tototai Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 RN
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh L.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalek U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.T.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20184747; PubMed=10721722; DOI=10.1016/S0378-1119(99)00499-0;
 RA Ching Y.-P., Qi Z., Wang J.H.;
 RT "Cloning of three novel neuronal Cdk5 activator binding proteins.";
 RL Gene 242:285-294(2000).
 CC -1- FUNCTION: Potential regulator of CDK5 activity. May be involved in
 CC cell proliferation. Regulates CDK5 activity via its interaction
 CC with CDK5R1 (By similarity).
 CC -1- SUBUNIT: Interacts with CDK5R1. This interaction is prevented by
 CC the association between CDK5R1 and CDK5RAP3 (By similarity).
 CC Interacts with the enteric adenovirus serotype 41 fiber protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q96JB5-1; Sequence=Displayed;
 CC Name=2; Synonyms=IC53;
 CC IsoId=Q96JB5-2; Sequence=VSP_007566, VSP_007567;
 CC Note=Due to an intron retention;
 CC Name=3; Synonyms=IC53-2;
 CC IsoId=Q96JB5-3; Sequence=VSP_007568;
 CC Note=Due to intron retention. No experimental confirmation
 CC available;
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Expressed in heart, brain,
 CC placenta, lung, liver, skeletal muscle, kidney and pancreas.
 CC Placenta 3 is expressed in kidney, liver, skeletal muscle and
 CC placenta.
 CC -1- PTM: Phosphorylated in vitro by CDK5 (By similarity).
 CC -1- SIMILARITY: Belongs to the CDK5RAP3 family.
 CC -1- CUIATION: Ref.3 sequence differs from that shown due to a
 CC frameshift in position 410.
 CC
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 CC -----
 DR EMBL: AF110322; AAC39277.1; -; mRNA.
 DR EMBL: AF217982; AAG17225.1; -; mRNA.
 DR EMBL: AF343090; AAK69655.1; -; ALT FRAMES; mRNA.
 DR EMBL: AB062433; BAB93496.1; -; mRNA.
 DR EMBL: AK023722; BAB14657.1; -; mRNA.
 DR EMBL: AK223387; BAD97107.1; -; mRNA.
 DR EMBL: BC009957; AAH09957.1; -; mRNA.
 DR EMBL: BC072435; AAH72435.1; -; mRNA.
 DR Ensembl: ENSG00000108465; Homo sapiens.
 DR HGNC: HGNC:18673; CDK5RAP3.
 DR MIM: 608202; gene.
 DR LinkHub: Q96JB5; -;
 DR GO: GO:0042808; F:neural Cdc2-like kinase binding; NMS.
 DR GO: GO:0007420; P:brain development; NMS.
 DR GO: GO:0008283; P:cell proliferation; ISS.
 DR GO: GO:0000079; P:regulation of cyclin dependent protein kina. .; ISS.
 DR GO: GO:0045664; P:regulation of neuron differentiation; NMS.
 DR InterPro: IPR006491; DUF773.
 DR InterPro: IPR013324; Sigma_t3_t4.
 DR PANTHER: PTHR14894; DUF773; 1.
 DR Pfam: PF05600; DUF773; 1.
 KW Alternative splicing; Phosphorylation.
 FT CHAIN
 FT 1 506 CDK5 regulatory subunit-associated
 FT protein 3.

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FT  VARSPIC 1 225 /FTid=PRO_0000220516.
FT  VARSPIC 1 87 Missing (in isoform 3).
FT  VARSPIC 1 87 Missing (in isoform 2).
FT  VARSPIC 88 111 /FTid=VSP_007566.
FT  VARSPIC 88 111 RYSSQRMKQWELIYKNDYTL -> MCVHPGACLPHV
FT  CONFLICT 113 113 /FTid=VSP_007567.
FT  CONFLICT 406 406 E -> V (in Ref. 6).
FT  CONFLICT 443 443 E -> K (in Ref. 3).
FT  CONFLICT 443 443 Q -> E (in Ref. 6).
SQ  SEQUENCE 506 AA; 56921 MW; A21E59A7E1F87E0 CRC64;

Query Match 18.3%; Score 70.5; DB 1; Length 506;
Best Local Similarity 29.5%; Pred. No. 20;
Matches 18; Conservative 5; Mismatches 19; Indels 19; Gaps 2;

QY 18 LEMGLVGAQKVSATDAPIR-----DWAFPPSFLCLPHRPAMTCSQAOPRGEKVG 71
DB 267 IDWGDFFGEAVSEGTDSGISAAAGIDWGIFFES-----DSKDPGGIDWG 313
QY 72 D 72
DB 314 D 314

RESULT 11
CKSP3_PONPY STANDARD; PRT; 506 AA.
AC QREX6;
DT 21-JUN-2005, integrated into UniProtKB/Swiss-Prot.
DT 21-DEC-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE CDK5 regulatory subunit-associated protein 3.
GN Name=CDK5RAP3;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
OX NCBI_TaxId=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RG The German cDNA consortium.
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Potential regulator of CDK5 activity. May be involved in
CC cell proliferation. Regulates CDK5 activity via its interaction
CC with CDK5R1 (By similarity).
CC -1- SUBUNIT: Interacts with CDK5R1. This interaction is prevented by
CC the association between CDK5R1 and CDK5RAP3 (By similarity).
CC -1- PTM: Phosphorylated in vitro by CDK5 (by similarity).
CC -1- SIMILARITY: Belongs to the CDK5RAP3 family.
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CC -----
DR EMBL: CR857387; CAH89681.1; -, mRNA.
DR InterPro: IPR008491; DUF773.
DR PANTHER: PTHR14894; DUF773; 1.
DR Pfam: PF05600; DUF773; 1.
DR KEGG: Phosphorylation.
FT CHAIN 1 506 CDK5 regulatory subunit-associated
FT protein 3
FT FTid=PRO_0000220518.
SQ SEQUENCE 506 AA; 56946 MW; E756A359FE5437D6 CRC64;

Query Match 18.3%; Score 70.5; DB 1; Length 506;
Best Local Similarity 29.5%; Pred. No. 20;
Matches 18; Conservative 5; Mismatches 19; Indels 19; Gaps 2;

QY 18 LEMGLVGAQKVSATDAPIR-----DWAFPPSFLCLPHRPAMTCSQAOPRGEKVG 71
DB 267 IDWGDFFGEAVSEGTDSGISAAAGIDWGIFFES-----DSKDPGGIDWG 313

```

```

QY 72 D 72
DB 314 D 314

RESULT 12
DCH_THAAR STANDARD; PRT; 257 AA.
AC 087873;
DT 24-OCT-2001, integrated into UniProtKB/Swiss-Prot.
DT 24-OCT-2001, sequence version 2.
DT 07-FEB-2006, entry version 27.
DE Cyclohexa-1,5-dienecarbonyl-CoA hydratase (EC 4.2.1.100) (Cyclohexa-
DE 1,5-diene-1-carboxyl-CoA hydratase) (Dienoyl-CoA hydratase).
GN Name=dch;
OS Thauera aromatica.
OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;
OC Rhodocyclaceae; Thauera.
OX NCBI_TaxId=59405;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=98417440; PubMed=9746358;
RA Breese K., Boll M., Alt-Moerbe J., Schaeffer H., Fuchs G.;
RT "Genes coding for the benzoyl-CoA pathway of anaerobic aromatic
RT metabolism in the bacterium Thauera aromatica.";
RL Eur. J. Biochem. 256:148-154(1998).
[2]
RP PROTEIN SEQUENCE OF 1-20, AND CHARACTERIZATION.
RX MEDLINE=98409281; PubMed=9738901;
RA Laempe D., Eisenreich W., Bacher A., Fuchs G.;
RT "Cyclohexa-1,5-diene-1-carboxyl-CoA hydratase, an enzyme involved in
RT anaerobic metabolism of benzoyl-CoA in the denitrifying bacterium
RT Thauera aromatica.";
RL Eur. J. Biochem. 255:618-627(1998).
CC -1- FUNCTION: Catalyzes the hydration of cyclohexa-1,5-diene-1-
CC carboxyl-CoA.
CC -1- CATALYTIC ACTIVITY: Cyclohexa-1,5-dienecarbonyl-CoA + H(2)O = 6-
CC hydroxycyclohex-1-enecarbonyl-CoA.
CC -1- PATHWAY: Aromatic compounds metabolism via benzoyl-CoA.
CC -1- SIMILARITY: Belongs to the enoyl-CoA hydratase/isomerase family.
CC -----
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CC -----
DR EMBL: AJ224959; CA112246.1; -, Genomic DNA.
DR InterPro: IPR001753; EnCoA_hydratase.
DR Pfam: PF00378; ECH; 1.
DR PROSITE: PS00166; ENOYL_COA_HYDRATASE; FALSE NEG.
KW Aromatic hydrocarbons catabolism; Direct protein sequencing; Lyase.
FT INT MET 0 257
FT CHAIN 1 257 Cyclohexa-1,5-dienecarbonyl-CoA
FT hydratase.
FT FTid=PRO_0000109323.
SQ SEQUENCE 257 AA; 27751 MW; 50FPAE61A868BF2C CRC64;

Query Match 18.1%; Score 70; DB 1; Length 257;
Best Local Similarity 28.6%; Pred. No. 12;
Matches 22; Conservative 11; Mismatches 30; Indels 14; Gaps 3;

QY 9 LTLILKSGCLEWGL-----VGAQKVSATDA-----PIRWAFPPSFLCLPHRPAMTCSQ- 60
DB 98 ILVALRQGCIGGGIVAAAGNLLEPAADAKFGQPEIRLGVFAPASCLLPRVGAACAD 157
QY 61 -----AOPRGEKVG 71
DB 158 LWMGSRSIDABEHRIG 174

RESULT 13
Q6IGC8_DROME PRELIMINARY; PRT; 130 AA.
AC Q6IGC8;

```

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE HCC06620.
 GN ORFNames=HDC06620;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peiryoeta;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r2;
 RA Hild M., Beckmann B., Haas S.A., Koch B., Solovjev V., Busold C.,
 RA Fellenberg K., Boutros M., Vingron M., Sauer F., Hohlseel J.D.,
 RA Paro R.;
 RT "an integrated gene annotation and transcriptional profiling approach
 RT towards the full gene content of the Drosophila genome.";
 RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 CC -----
 DR EMBL; BK003838; DAA02536.1; -; Genomic DNA.
 SQ SEQUENCE 130 AA; 14460 MW; 34195AF7682CAFD7 CRC64;
 Query Match 18.0%; Score 69.5; DB 2; Length 130;
 Best Local Similarity 30.7%; Pred. No. 7;
 Matches 27; Conservative 7; Mismatches 19; Indels 35; Gaps 5;
 QY 4 LTTLLLLKSGLENGVCAQKVSATD-----APL-RDM-AFFPP----- 44
 Db 12 MLTLLLLLRGRCRRSMGNCNNNNHAAKNNFSLMTATGRTWAPFPPEPMVEYDPE 71
 QY 45 -----SFLCLLP-HRPAM 56
 Db 72 VDVPHLDLNSQLANGMMLPGHVPAL 99
 RESULT 14
 ID KREM2_HUMAN STANDARD; PRT; 462 AA.
 AC Q8NCW0; Q8NC2J4; Q8NCW1; Q96GL8; Q9BRP9;
 DT 23-APR-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 27.
 DE Kremen protein 2 precursor (Kring)-containing protein marking the eye
 DE and the nose) (Dickkopf receptor 2).
 GN Name=KREM2; Synonyms=KRM2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (mRNA), AND ALTERNATIVE SPLICING.
 RA Tanaka S., Sugimachi K.;
 RT "Human Kremen2 and Wnt signaling.";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 3 AND 4).
 RC TISSUE=Ovarian carcinoma;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai T., Isono Y., Nakamura Y., Nagahara K.,
 RA Murakami K., Yasuda K., Iwayanagi T., Wagatsuna M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M., Yamazaki M.,

RA Ninomiya K., Ishibashi T., Yamaehta H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotta T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Mueselino K., Iwaki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshihara Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nishigaki S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujikawa T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsunuma K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hara H., Watanabe M., Komatsu T.,
 RA Mutsaers-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamaehta R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isozaki T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 3 AND 4).
 RC TISSUE=Brain, and Uterus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
 RA Stajich E.L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stajich E.L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Bata S.S., Loguelfo N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gutierrez P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhe D.E.,
 RA Scherch J., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
 CC to block Wnt/beta-catenin signaling. Forms a ternary complex with
 CC Dkk1 and LRP6 and induces rapid endocytosis and removal of the Wnt
 CC receptor LRP6 from the plasma membrane (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
 CC protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q8NCW0-1; Sequence=Displayed;
 CC Name=2; Synonyms=Kremen2a;
 CC IsoId=Q8NCW0-2; Sequence=VSP_050509, VSP_050510;
 CC Name=3; Synonyms=Kremen2b;
 CC IsoId=Q8NCW0-3; Sequence=VSP_050511, VSP_050512;
 CC Name=4; Synonyms=Kremen2c;
 CC IsoId=Q8NCW0-4; Sequence=VSP_050513, VSP_050514;
 CC -1- SIMILARITY: Contains 1 CUB domain.
 CC -1- SIMILARITY: Contains 1 kring domain.
 CC -1- SIMILARITY: Contains 1 WSC domain.
 CC -----
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 CC -----
 DR EMBL; AB086405; BAC00872.1; -; mRNA.
 DR EMBL; AB086355; BAC00823.1; -; mRNA.
 DR EMBL; AB086356; BAC00824.1; -; mRNA.

DR	EMBL	AB086357	BAC00825.1	-	-	mRNA.
DR	EMBL	AK027669	BAB55281.1	-	-	mRNA.
DR	EMBL	AK075033	BAC11365.1	-	-	mRNA.
DR	EMBL	BC003533	AAH03533.1	-	-	mRNA.
DR	EMBL	BC009383	AAH09383.1	-	-	mRNA.
DR	HSSP	P00750	1PK2			
DR	Ensembl	ENSG00000131650	Homo sapiens.			
DR	HGNC	HGNC:18797	KREMEN2			
DR	InterPro	IPR000859	CUB			
DR	InterPro	IPR000001	Kringle			
DR	InterPro	IPR002889	WSC_carb_bd			
DR	Pfam	PF00431	CUB	1		
DR	Pfam	PF00051	Kringle	1		
DR	Pfam	PF01822	WSC	1		
DR	PRINTS	PR00018	KRINGLE			
DR	ProDom	PD000395	Kringle	1		
DR	SMART	SM00042	CUB	1		
DR	SMART	SM00130	KR	1		
DR	PROSITE	PS01180	CUB	1		
DR	PROSITE	PS00021	KRINGLE_1	1		
DR	PROSITE	PS50070	KRINGLE_2	1		
KW	Alternative splicing	Glycoprotein; Kringle; Membrane; Signal;				
KW	Transmembrane	Wnt signaling pathway.				
FT	SIGNAL	1	25			Potential..
FT	CHAIN	26	462			Kremen protein 2.
FT	TOPO_DOM	26	364			/FTid=PRO_0000021568.
FT	TRANSMEM	365	387			Extracellular (Potential).
FT	TOPO_DOM	388	462			Potential.
FT	DOMAIN	35	119			Cytoplasmic (Potential).
FT	DOMAIN	121	215			Kringle.
FT	DOMAIN	219	326			WSC.
FT	CARBOHYD	49	49			CUB.
FT	CARBOHYD	222	222			N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	244	244			N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	351	351			N-linked (GlcNAc. . .) (Potential).
FT	DISULFID	36	119			By similarity.
FT	DISULFID	89	100			By similarity.
FT	DISULFID	119	114			By similarity.
FT	DISULFID	219	245			By similarity.
FT	VARSPLIC	367	420			AVPSTVTAVSVTLTLGLRLPLRRSLGAKGKPPALG
FT						AARGPRRSAAWT -> GAVCWIREKGPRRWGLPGAPGZAG
FT						LCGINSPEGMPCGAPPGTFLRLVLPRTGL (in isoform 3).
FT						/FTid=VSP_050511.
FT	VARSPLIC	367	399			AAVPSVTAVSVTLTLGLRLPLRRSLCLAP -> GEAG
FT						AADGSSGSRPLAFLITAAVCPQPSRR (in isoform 4).
FT						/FTid=VSP_050513.
FT	VARSPLIC	394	424			SCILAPWGKPPALGASRGPRRSAAVWVQQPR -> CGALGO
FT						GLRADPWGAGAPAGNRRAREKLIGS (in isoform 2).
FT						/FTid=VSP_050509.
FT	VARSPLIC	400	462			Missing (in isoform 4).
FT						/FTid=VSP_050514.
FT	VARSPLIC	421	462			Missing (in isoform 3).
FT						/FTid=VSP_050512.
FT	VARSPLIC	425	462			Missing (in isoform 2).
FT						/FTid=VSP_050510.
FT	CONFLICT	164	202			Missing (in Ref. 2; BAC11365).
FT	CONFLICT	285	285			A -> D (in Ref. 2; BAC11365).
FO	SEQUENCE	462 AA	48849 MW			CE33015917A9A68 CRC64;

Query Match	Similarity	Score	DB 1	Length	462
Best Local	Similarity 33.8%	Pred No 27			
Matches	24	Conservative	7	Mismatches	34
				Indels	6
				Gaps	2
QY	1	MLLTLLTLLTLLKSGSCEMLGVGAQVSSAIDAPLRDWAFFPSPSTCLIPHRPMTCSG	60		
DB	379	LTLLLTGLLRPRRRRCILAPGKGPAL--GASGPRRSMWVYQ-----PRGVLPSP	432		
QY	61	APRGEGERKV 71			
DB	433	GDPOAEGSNAG 443			

RESULT 15

QARTS7_TETNG PRELIMINARY: PRT: 652 AA.

QARTS7_TETNG

19-JUL-2005, integrated into UniProtKB/TrEMBL.

QARTS7

19-JUL-2005, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Chromosome 2 SCAR14997, whole genome shotgun sequence. (Fragment).

CN ORFNames=STENSG0029115001.

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

NCBI_TaxID=99883;

NP Nucleotide Sequence.

NP Published-15496914; DOI=10.1038/nature03025;

RX Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N., Mauceli E., Bonnaud L., Fischer C., Ozouf-Costaz C., Bernot A., Naud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Daslav C., Salanoubat M., Levy M., Bondet N., Vachellerie B., Anthouard C., Jubin C., Castelli V., Kainka M., Vachellerie B., Blemont C., Skalli Z., Catcollito L., Poulain J., De Berardinis V., Craud C., Duprat S., Brottier P., Coutencan J.-P., Gouzy J., Parra G., Landier G., Chapelle C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volf J.-N., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Landet V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Landier E.S., Weissbach J., Roest Crollius H., et al. "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";

RT Nature 431:946-957(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research; Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.

CC -! CAUTION: The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC -! SIMILARITY: Belongs to the ABC transporter family.

CC -----

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CC -----

CC EMBL: CAAE01014997; CAG08205.1; -! Genomic DNA.

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0005524; F:ATP binding; IEA.

DR GO: GO:0016887; F:ATPase activity; IEA.

DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. .; IEA.

DR GO: GO:0006810; P:transport; IEA.

DR GO: GO:0000166; P:nucleotide binding; IEA.

DR InterPro: IPR003593; AAA ATPase.

DR InterPro: IPR011527; ABC_TM_1.

DR InterPro: IPR003439; ABC_transp_like.

DR Pfam: PF00664; ABC_membrane; 1.

DR Pfam: PF00005; ABC_tran; 1.

DR ProDom: PD000006; ABC_transporter; 1.

DR SMART: SM00382; AAA; 1.

DR PROSITE: PS00929; ABC_TM1F; 1.

DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.

DR PROSITE: PS00893; ABC_TRANSPORTER_2; 1.

KW ATP-binding; Nucleotide-binding.

FT NON_TER 1

FT TER 652

SEQUENCE 652 AA; 72132 MW; 515BDEFCDFF1515 CRC64;

Query Match	17.9%	Score 69;	DB 2;	Length 652;
Best Local Similarity	56.7%	Pred. No. 38;		
Matches 17;	Conservative 0;	Mismatches 7;	Indels 6;	Gaps 2;

Qy	44	PSFLCLPHRPAWTCQAQPRGEGKVG	73
Db	450	PSLCLLPH-VATCS-----GSEBPAGPG	473

Search completed: June 6, 2006, 21:38:37
Job time : 297 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 21:33:55 ; Search time 39 Seconds
(without alignments)
180.098 Million cell updates/sec

Title: US-10-063-534-30
Perfect score: 386
Sequence: I MLTLTLTLTLTLKSGCLEW.....PAMTCQAOPRGEKVG 73

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70.5	18.3	419	2 J07863	IC53 protein - hum
2	67.5	17.5	669	2 A49585	Na ⁺ channel protei
3	65.5	17.0	3788	2 T13960	belgie protein Homo
4	63.5	16.5	277	2 I52825	gene MAC25 protein
5	63.5	16.5	278	2 T46458	hypothetical prote
6	63.5	16.5	282	2 S50031	prostacyclin-stimu
7	63	16.3	141	1 HARNW	hemoglobin alpha c
8	63	16.3	141	2 A25477	hemoglobin alpha c
9	62.5	16.2	270	2 S56160	mast cell tryptase
10	62.5	16.2	283	2 B83618	probable CoA trans
11	62	16.1	141	2 A23571	hemoglobin alpha c
12	62	16.1	496	1 C4B0C2	steroid 21-monooxy
13	62	16.1	1240	1 D1BE21	DNA-directed DNA p
14	61.5	15.9	148	2 AB3004	hypothetical prote
15	61.5	15.9	148	2 G98279	hypothetical prote
16	61.5	15.9	326	2 AB3100	hypothetical prote
17	61.5	15.9	326	2 H98186	probable mikropin
18	61.5	15.9	365	2 JH0534	class I histococpa
19	61	15.8	784	2 J00317	hypothetical 82K p
20	60.5	15.7	273	1 HAHUW	MHC class I histoc
21	60.5	15.7	273	1 HAHUW	MHC class I histoc
22	60.5	15.7	274	1 HAHUJ2	MHC class I histoc
23	60.5	15.7	275	1 HAHUJ0	MHC class I histoc
24	60.5	15.7	357	2 S18198	class I histococpa
25	60.5	15.7	365	1 HAHUJ2	MHC class I histoc
26	60.5	15.7	365	2 I18443	gene HLA-A-0203 pr
27	60.5	15.7	365	2 A45847	MHC class I histoc
28	60.5	15.7	365	2 I61902	MHC class I histoc
29	60.5	15.7	365	2 I18441	gene HLA-A-6802 pr

30	60.5	15.7	365	2 I37470	HLA-A*0210 - human
31	60.5	15.7	365	2 I84448	MHC class I histoc
32	60.5	15.7	365	2 JH0536	class I histococpa
33	60.5	15.7	365	2 I37477	MHC class I histoc
34	60.5	15.7	365	2 I37483	HLA-A*34.2 antigen
35	60.5	15.7	365	2 I37482	MHC class I histoc
36	60.5	15.7	365	2 I61857	MHC class I histoc
37	60.5	15.7	365	2 I38442	gene HLA-A-0205 pr
38	60	15.5	142	1 HAMS	hemoglobin alpha c
39	60	15.5	492	1 A32525	steroid 21-monooxy
40	59.5	15.4	317	2 I46916	insulin-like growt
41	59.5	15.4	365	2 I37542	MHC class I histoc
42	59.5	15.4	365	2 JH0535	class I histococpa
43	59.5	15.4	365	2 JLO135	MHC class I histoc
44	59.5	15.4	446	2 A34794	B-cell CLL/Lymphom
45	59.5	15.4	1805	2 A34736	nestin - rat

ALIGNMENTS

RESULT 1
JC7863
IC53 protein - human
C/Species: Homo sapiens (man)
C/Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 21-Apr-2003
C/Accession: JC7863

R/Chen, J.; Liu, B.; Liu, Y.; Han, Y.; Yu, H.; Zhang, Y.; Lu, L.; Zhen, Y.; Hui, R.
Biochem. Biophys. Res. Commun. 294, 161-166, 2002
A/Title: A novel gene IC53 stimulates EC9304 cell proliferation and is upregulated in fa
A/Reference number: JC7863; MUID:22050200; PMID:12054757
A/Accession: JC7863
A/Molecule type: mRNA
A/Residues: 1-419 <CHE>
A/Cross-references: UNIPARC:UP100000723B0; GB:AF10322
C/Comment: This protein, a homolog of C53 protein, is an intracellular protein. It is a r
formation in blood-deprived heart tissues.
C/Genetics:
A/Gene: ic53
A/Map position: 17q21.31
C/Keywords: cardiac muscle, heart

Query Match 18.3%; Score 70.5; DB 2; Length 419;
Best Local Similarity 29.5%; Pred. No. 1.7;
Matches 18; Conservative 5; Mismatches 19; Indels 19; Gaps 2;

QY 18 LEMGLVGAQKVSAATDAPIR-----DWAPPPSEFLCLPHRPAMTCQAOPRGEKVG 71
DB 180 IDWQDFGVEAVSEGTDSGISAEAAIDWGIFFPS-----DSKDPGGDGIW 226

QY 72 D 72
DB 227 D 227

RESULT 2
A49585
Na⁺ channel protein, amiloride-sensitive - human
C/Species: Homo sapiens (man)
C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C/Accession: A49585; I51911
R/Voillay, N.; Lingueglia, B.; Champigny, G.; Mattei, M.G.; Waldmann, R.; Lazdunski, M.;
Proc. Natl. Acad. Sci. U.S.A. 91, 247-251, 1994
A/Title: The lung amiloride-sensitive Na⁺ channel: biophysical properties, pharmacology,
A/Reference number: A49585; MUID:9410514; PMID:8278374
A/Accession: A49585
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-669 <RES>
A/Cross-references: UNIPROT:P37088; UNIPARC:UP10000000DC4; EMBL:X76180; NID:g452649; PIDR
R/McDonald, F.J.; Snyder, P.M.; McCray, P.B.
Am. J. Physiol. 266, L728-L734, 1994
A/Title: Cloning, expression, and tissue distribution of a human amiloride-sensitive Na⁺

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A:Reference number: I51911; MUID:944295729; PMID:8023962
A:Accession: I51911
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-669 <RES>
A:Cross-references: UNIPARC:UPI000000DDC4; GB:L29007; NID:g493125; PIDN:AAA21813.1; PID:
C:Genetics:
A:Map position: 12p13
C:Superfamily: human amiloride-sensitive sodium channel protein; fibronectin type I repeat
Query Match 17.5%; Score 67.5; DB 2; Length 669;
Best Local Similarity 33.8%; Pred. No. 5.9;
Matches 22; Conservative 9; Mismatches 21; Indels 13; Gaps 3;
OY 3 LTTLLTLLILKSGCLEW----GLVGAQKVSATDAPIRDMAFPPSPFLCLPHRPAMTC 58
DB 576 LTVVFMFLMLLRFRSRYSRSGRGAEVASTL-----ASSPPSHFC--PPMWSLST 626
OY 59 SQAQP 63
DB 627 SQGP 631
RESULT 3
T13960
beige protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13960
R:Motif, M.: Nishikawa, T.; Higuchi, K.; Nishimura, M.
submitted to the EMBL Data Library, November 1998
A:Description: Deletion in the beige gene of the beige rat due to recombination between
A:Reference number: Z17837
A:Accession: T13960
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-3788 <MOR>
A:Cross-references: UNIPROT:Q922X9; UNIPARC:UPI000005B7B; EMBL:AB020019; NID:d1241953;
A:Experimental source: strain DA; spleen
C:Genetics:
A:Gene: beige
Query Match 17.0%; Score 65.5; DB 2; Length 3788;
Best Local Similarity 33.8%; Pred. No. 52;
Matches 22; Conservative 9; Mismatches 25; Indels 9; Gaps 3;
OY 4 LTTLLTLLILKSGCLEWGLVGAQKVSATDAPIRDMAFPPSPFLCL-LPHRPAMT--CSQ 60
DB 1349 LTLILRIFLERSPTETILHGIQKIVES-----DFTMSPSQYLTFFILHPTLSNGVSS 1402
OY 61 AOPRG 65
DB 1403 QKPPG 1407
RESULT 4
I52825
gene MAC25 protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C:Accession: I52825
R:Murphy, M.; Pyke, M.; Harnish, P.; Zang, K.D.; George, D.L.
Cell Growth Differ. 4, 715-722, 1993
A:Title: Identification and characterization of genes differentially expressed in meningioma
A:Reference number: I52825; MUID:94059820; PMID:7694637
A:Accession: I52825
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: UNIPROT:Q16270; UNIPARC:UPI000016ACE; GB:L19182; NID:g307150; PIDN:
C:Genetics:
A:Gene: MAC25
C:Superfamily: IGBBP-related protein, MAC25 type; Kazal protease inhibitor homology

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F:104-156/Domain: Kazal proteinase inhibitor homology <KPI8>

Query Match      16.5%; Score 63.5; DB 2; Length 277;
Best Local Similarity 38.6%; Pred. No. 7.5;
Matches 27; Conservative 1; Mismatches 29; Indels 13; Gaps 3;

OY 6 LLLLLLLKSGSLEWGLVGAQKVSATDAPIRDMAFFP-PSFLCLLPH-RPAMTCSQAQP 63
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 16 LLLLLLPLSSSS-----SSDTGCFEFASCPPLPLGLCLGELTRDACCCEPMCA 64
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 64 RGEGERKVDG 73
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 RGEGERCGGG 74
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
T46458
hypothetical protein DKFZp434M102.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46458
R:Ansoerg, W.; Wirkner, U.; Wewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223028
A:Accession: T46458
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-278 <AAA>
A:Cross-references: UNIPROT:Q9NTB5; UNIPARC:UPI000007047B; EMBL:AL137404
A:Experimental source: adult testis; clone DKFZp434M102
A:Genetics:
A>Note: DKFZp434M102.1

Query Match      16.5%; Score 63.5; DB 2; Length 278;
Best Local Similarity 24.2%; Pred. No. 7.5;
Matches 24; Conservative 1; Mismatches 29; Indels 35; Gaps 4;

OY 2 LLLLLLLLLL-----KSGSLEWGLV-----GAQKVSAA 31
    : ||| : | | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 84 MLTFELVLVLTATLCTRLHRNFRGBSIYWGTPADSDTVAGEFPPTPRGPRPTSR 143
    : ||| : | | | : | | : | | : | | : | | : | | : | | : | | : | |

OY 32 TDAPTRDMAFFPSPFLCLPHRPAMTCSQAQPRGEGKV 70
    ||| : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 144 PAAP-RSPALPP---LTRRPAHSCAEAAASAKRV 177
    ||| : | | : | | : | | : | | : | | : | | : | | : | | : | |

RESULT 6
S50031
proteacyclin-stimulating factor - human
C:Species: Homo sapiens (man)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
C:Accession: S50031
R:Yamuchi, T.; Umeda, F.; Maekado, M.; Isaji, M.; Mizushima, S.; Nawata, H.
Biochem. J. 303, 591-598, 1994
A:Title: Purification and molecular cloning of proteacyclin-stimulating factor from serum
A:Reference number: S50031; MUID:95071263; PMID:7980422
A:Accession: S50031
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-282 <YAM>
A:Cross-references: UNIPROT:Q16270; UNIPARC:UPI00000422D2; GB:S75725; NID:9861520; PIDN:4;
C:Superfamily: IGF1P-related protein, MAC25 type, Kazal proteinase inhibitor homology
F:104-156/Domain: Kazal proteinase inhibitor homology <KPI8>

Query Match      16.5%; Score 63.5; DB 2; Length 282;
Best Local Similarity 38.6%; Pred. No. 7.6;
Matches 27; Conservative 1; Mismatches 29; Indels 13; Gaps 3;

OY 6 LLLLLLLKSGSLEWGLVGAQKVSATDAPIRDMAFFP-PSFLCLLPH-RPAMTCSQAQP 63
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 16 LLLLLLPLSSSS-----SSDTGCFEFASCPPLPLGLCLGELTRDACCCEPMCA 64
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 64 RGEGERKVDG 73
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 65 RGESEPCGGG 74

RESULT 7

HARRM

hemoglobin alpha chain - white rhinoceros
C:Species: Ceratotherium simum (white rhinoceros, square-lipped rhinoceros)
C:Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 12-Jul-2004
C:Accession: A02286
R:Matuz, G.; Braunitzer, G.; Wright, P.G.
Hope-Seyler's Z. Physiol. Chem. 363, 1077-1085, 1982
A:Title: Die Primärstruktur des Hemoglobins vom Breitmaulnashorn (Ceratotherium simum,
A:Reference number: A91701; PMID:83055102; PMID:7141412
A:Accession: A02286
A:Molecule type: protein
A:Residues: 1-141 <MAZ>
A:Cross-references: UNIPROT:P01963; UNIPARC:UPI000012C15E
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrier
F:2-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 16.3%; Score 63; DB 1; Length 141;
Best Local Similarity 35.8%; Pred. No. 4.6;
Matches 19; Conservative 7; Mismatches 25; Indels 2; Gaps 2;

20 WGLVGAQKVSATDAPIRDMAFPPPSFLCLPHRPAMTCSQAOPRGEKGYD 72

14 WGHVGAQAGEYGAEALERMFLSPPT-KTYFPHPD-LSHGSAQYKAGHKVAD 64

RESULT 8

A23477

hemoglobin alpha chain - white-faced sapsajou
C:Species: Cebus capucinus (white-faced sapsajou, white-throated capuchin)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 12-Jul-2004
C:Accession: A25477
R:Timika, Y.; Araya, A.; Maite, T.; Matsuda, G.
Biol. Chem. Hoppe-Seyler 367, 147-152, 1986
A:Title: Primary structure of adult hemoglobin of white-throated capuchin, Cebus capucinus
A:Reference number: A90702; PMID:86187258; PMID:3964444
A:Accession: A25477
A:Molecule type: protein
A:Residues: 1-141 <TAN>
A:Cross-references: UNIPROT:P07421; UNIPARC:UPI000012C15C
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; heme; iron; metalloprotein; oxygen carrier
F:2-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 16.3%; Score 63; DB 2; Length 141;
Best Local Similarity 35.8%; Pred. No. 4.6;
Matches 19; Conservative 6; Mismatches 26; Indels 2; Gaps 2;

20 WGLVGAQKVSATDAPIRDMAFPPPSFLCLPHRPAMTCSQAOPRGEKGYD 72

14 WGVGAHAGDYGDALERMFLSPPT-KTYFPHPD-LSHGSAQYKAGHKVAD 64

RESULT 9

S56160

maest cell tryptase precursor - Mongolian jird
C:Species: Meriones unguiculatus (Mongolian jird)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S56160
R:Murakumo, Y.; Ide, H.; Itoh, H.; Tomita, M.; Kobayashi, T.; Maruyama, H.; Horii, Y.; N
Biochem. J. 309, 921-926, 1995
A:Title: Cloning of the cDNA encoding maest cell tryptase of Mongolian gerbil, Meriones u
A:Reference number: S56160; PMID:95366971; PMID:7639711
A:Accession: S56160

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-270 <MR>
A:Cross-references: UNIPROT:P50342; UNIPARC:UPI000013771D; EMBL:D31789; NID:9517122; PID
F:26-262/Domain: trypsin homology <TRY>

Query Match 16.2%; Score 62.5; DB 2; Length 270;
Best Local Similarity 40.0%; Pred. No. 9.6;
Matches 16; Conservative 5; Mismatches 12; Indels 7; Gaps 2;

1 MLITLTLTLTLKGS-CLEWGLVGAQKVSATDAPIRDW 39

4 LTLTLPLFLMHRSPICQEWGIVGQ-----EAPGNKV 37

RESULT 10

B83618

probable CoA transferase, subunit A PA0226 [imported] - Pseudomonas aeruginosa (strain P
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83618
R:Stover, C.K.; Pham, X.Q.; Ervin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A:Reference number: A82950; PMID:20437337; PMID:10984043
A:Accession: B83618
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-283 <STO>
A:Cross-references: UNIPROT:Q916R2; UNIPARC:UPI000004C4FA9; GB:AE004460; GB:AE004091; NID
A:Experimental source: strain PA01
A:Genetics:
A:Gene: PA0226

Query Match 16.2%; Score 62.5; DB 2; Length 283;
Best Local Similarity 29.3%; Pred. No. 10;
Matches 17; Conservative 7; Mismatches 11; Indels 23; Gaps 3;

14 KGSCLWGLVGAQK-----VSATDAPIR----DMAFPSPFLCLIP 51

171 KANVLWGIQVGEALAAKRCIVAEIVDELDAFMACVLPSPMAL---SAVCLVP 225

RESULT 11

A23571

hemoglobin alpha chain - southeastern quoll
C:Species: Dasyurus viverrinus (southeastern quoll)
C:Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 12-Jul-2004
C:Accession: A23571
R:Matwright, B.; Hope, R.
Proc. Natl. Acad. Sci. U.S.A. 82, 8105-8108, 1985
A:Title: Cloning and chromosomal location of the alpha- and beta-globin genes from a mars
A:Reference number: A94077; PMID:86068050; PMID:3865220
A:Accession: A23571
A:Molecule type: mRNA
A:Residues: 1-141 <MAI>
A:Cross-references: UNIPROT:P07419; UNIPARC:UPI000012C171; GB:M14567; NID:G163892; PIDN:
A:Note: Initiator Met not shown
C:Superfamily: globin; globin homology
C:Keywords: blood; chromoprotein; heme; iron; metalloprotein; oxygen carrier
F:2-141/Domain: globin homology <GLB>
F:58/Binding site: oxygen (His) (distal axial ligand) #status predicted
F:87/Binding site: heme iron (His) (proximal axial ligand) #status predicted

Query Match 16.1%; Score 62; DB 2; Length 141;
Best Local Similarity 34.0%; Pred. No. 6;
Matches 19; Conservative 8; Mismatches 25; Indels 2; Gaps 2;

20 WGLVGAQKVSATDAPIRDMAFPPPSFLCLPHRPAMTCSQAOPRGEKGYD 72

14 WGLVGAQKVSATDAPIRDMAFPPPSFLCLPHRPAMTCSQAOPRGEKGYD 72

Db 14 WKGVGHAGAGAAEALARTLSPPTT-KTYEPHFD-LSPGSAIQGHKKVAD 64

RESULT 12

stereoid 21-monooxygenase (EC 1.14.99.10) cytochrome P450 21A1 - bovine
N/Alternate names: cytochrome P450 (C21); steroid 21-hydroxylase

C/Species: Bos primigenius taurus (cattle)

C/Date: 28-May-1986 #sequence revision 05-Apr-1995 #text_change 09-Jul-2004

C/Accession: A27555; A00192; A24101; C28600; A21181

R/Chung, B.; Matleson, K.J.; Miller, W.L.

Proc. Natl. Acad. Sci. U.S.A. 83, 4243-4247, 1986

A/Title: Structure of a bovine gene for P-450C21 (steroid 21-hydroxylase) defines a novel

A/Reference number: A27555; MUID:86233409; PMID:3487086

A/Accession: A27555

A/Molecule type: DNA

A/Residues: 1-496 <CHU>

A/Cross-references: UNIPROT:P00191; UNIPARC:UP1000012826; GB:M1267; NID:g163466; PIDN:

R/Yoshioka, H.; Morohashi, K.; Sogawa, K.; Yamane, M.; Komitani, S.; Takemori, S.; Okada

J. Biol. Chem. 261, 4106-4109, 1986

A/Title: Structural analysis of cloned cDNA for mRNA of microsomal cytochrome P-450 (C21)

A/Reference number: A00192; MUID:86140226; PMID:3005319

A/Accession: A00192

A/Molecule type: mRNA

A/Residues: 1-13, 'S', '15-400, 'Y', '402-496 <YOS>

A/Cross-references: UNIPARC:UP10000167C38; GB:M12918; NID:g162947; PIDN:AAA30487.1; PID:

A/Experimental source: adrenal cortex microsomes

R/John, M.E.; Okamura, T.; Dee, A.; Adler, B.; John, M.C.; White, P.C.; Simpson, E.R.; W

Biochemistry 25, 2846-2853, 1986

A/Title: Bovine steroid 21-hydroxylase: regulation of biosynthesis.

A/Reference number: A24101; MUID:86243279; PMID:2424492

A/Accession: A24101

A/Molecule type: mRNA

A/Residues: 121-430 'C', '432-496 <JOH>

A/Cross-references: UNIPARC:UP100001662F3; GB:K01333; NID:g162944; PIDN:AAA30486.1; PID:

R/Ogishima, T.; Okada, Y.; Komitani, S.; Takemori, S.; Omura, T.

J. Biochem. 94, 1711-1714, 1983

A/Title: Partial amino acid sequences of two mitochondrial and two microsomal cytochrome

A/Reference number: A91972; MUID:84087829; PMID:6654880

A/Accession: C28600

A/Molecule type: Protein

A/Residues: 1-12, 'K', '14-15, '248-250, 'S' <OGS>

A/Cross-references: UNIPARC:UP10000171D8D

A/Experimental source: adrenal cortex microsomes

R/White, P.C.; New, M.I.; Dupont, B.

Proc. Natl. Acad. Sci. U.S.A. 81, 1986-1990, 1984

A/Title: Cloning and expression of cDNA encoding a bovine adrenal cytochrome P-450 spec

A/Reference number: A21181; MUID:84193940; PMID:6603358

A/Contents: annotation; sequence report

A/Note: this sequence differs substantially from that in reference A24101

C/Genetics:

A/Insertion: 68/1; 98/1; 149/3; 181/3; 215/3; 244/3; 311/3; 371/2; 406/1

C/Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

C/Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo

F/287-449/Domain: cytochrome P450 homology <P45>

F/427/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 16.1%; Score 62; DB 1; Length 496;

Best Local Similarity 37.9%; Pred. No. 19;

Matches 25; Conservative 6; Mismatches 25; Indels 10; Gaps 3;

QY 1 MLLTLLTLLTLLKSGCLEWGLVGAQKVSSATDAPIRDMAFPPSPFLCL-PPHPAMTCS 59

Db 1 MVLGLGLTLLTLLAGAHLLW---GRWKLRLHLPL-----VPGFLTLQPNPIHLLS 51

QY 60 QAQPRG 65

Db 52 LTQKLG 57

RESULT 13

DJBR21
DNA-directed DNA polymerase (EC 2.7.7.7) - human herpesvirus 2 (strain 186)

C/Species: human herpesvirus 2

C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C/Accession: A27315

R/Tsurumi, T.; Maeno, K.; Nishiyama, Y.

Gene 52, 129-137, 1987

A/Title: Nucleotide sequence of the DNA polymerase gene of herpes simplex virus type 2 at

A/Reference number: A27315; MUID:87277385; PMID:3038677

A/Accession: A27315

A/Molecule type: DNA

A/Residues: 1-1240 <TSU>

A/Cross-references: UNIPROT:P07918; UNIPARC:UP10000129807; GB:M16321; NID:g330291; PIDN:

C/Superfamily: DNA polymerase

C/Keywords: DNA binding; DNA replication; nucleotidyltransferase

Query Match 16.1%; Score 62; DB 1; Length 1240;

Best Local Similarity 56.5%; Pred. No. 46;

Matches 13; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 51 PHRPAMTCSQAQPRGEGEKVGDG 73

Db 652 PKRPAV-----PRGEGERPDDG 668

RESULT 14

AB3004
hypotheoretical protein Atu3636 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C/Accession: AB3004

R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McCellig

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I

ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; MUID:21608550; PMID:11743193

A/Accession: AB3004

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-148 <KUR>

A/Cross-references: UNIPROT:Q8U9T9; UNIPARC:UP10000002299; GB:AE086889; PIDN:AAL44448.1;

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Map position: linear chromosome

Query Match 15.9%; Score 61.5; DB 2; Length 148;

Best Local Similarity 29.0%; Pred. No. 7.1;

Matches 20; Conservative 14; Mismatches 14; Indels 21; Gaps 4;

QY 10 LLLKSGCLEWGLVGAQKVSSATDAPIRDMAFPPSPFLC-----LLPHRPM----- 56

Db 1 MILVEGKTLFF---GDORVSA--SPWRKRPSSAMNLFVLDINKPGVRPHRPLLSACUR 55

QY 57 ---TCGSAQ 62

Db 56 TLHSCSDVE 64

RESULT 15

G98279
hypotheoretical protein AGR_L_2383 [imported] - Agrobacterium tumefaciens (strain C58, Cerec

C/Species: Agrobacterium tumefaciens

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C/Accession: G98279

R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;

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